

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 21:50:17 ; Search time 2304 Seconds  
(without alignments)  
9199.107 Million cell updates/sec

Title: US-09-773-476-294  
Perfect score: 489  
Sequence: 1 gactgagctagatcttcag.....tnatgagccacacaagactt 489

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues  
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
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32: em\_htg\_other.\*  
33: em\_htg\_mus.\*  
34: em\_htg\_pin.\*  
35: em\_htg\_rod.\*  
36: em\_htg\_mam.\*  
37: em\_htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	471.4	96.4	979	10	BC057097	BC057097 Mus muscu
2	470.4	96.2	896	10	BC049637	BC049637 Mus muscu
3	353	72.2	905	6	BD076403	BD076403 Human pro
4	353	72.2	922	9	BC002846	BC002846 Homo sapi
5	353	72.2	932	6	AX055686	AX055686 Sequence
6	353	72.2	932	6	AX076904	AX076904 Sequence
7	353	72.2	932	6	AX077021	AX077021 Sequence
8	353	72.2	932	6	AX574480	AX574480 Sequence
9	353	72.2	932	9	AY358968	AY358968 Homo sapi
10	353	72.2	940	9	BC011006	BC011006 Homo sapi
11	353	72.2	970	9	BC035850	BC035850 Homo sapi
12	353	72.2	1056	9	BC021237	BC021237 Homo sapi
13	353	72.2	1265	6	BD276564	BD276564 EXTRACELL
14	353	72.2	1265	6	AX048198	AX048198 Sequence
15	351.4	71.9	915	9	AF275744	AF275744 Homo sapi
16	344	70.3	687	6	BD076393	BD076393 Human pro
17	340.4	69.6	1074	9	AF144055	AF144055 Homo sapi
18	287.6	58.8	512	6	AX395873	AX395873 Sequence
19	256.2	52.4	549	6	AX395797	AX395797 Sequence
20	254.6	52.1	529	6	AX778895	AX778895 Sequence
21	182.6	37.3	524	6	AR413766	AR413766 Sequence
22	182.6	37.3	524	6	BD109319	BD109319 EST and e
23	173.2	35.4	486	6	AX552302	AX552302 Sequence
24	165	33.7	498	6	AR415192	AR415192 Sequence
25	165	33.7	498	6	BD110745	BD110745 EST and e
26	146.8	30.0	459	6	AX884298	AX884298 Sequence
27	146.8	30.0	459	6	BD023908	BD023908 Sequence
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30	123.8	25.3	209211	2	AC084883	AC084883 Mus muscu
31	123.8	25.3	216195	10	AC109608	AC109608 Mus muscu
32	113.6	23.2	180005	2	AC112904	AC112904 Rattus no
33	113.6	23.2	264108	2	AC126142	AC126142 Rattus no
34	113.6	23.2	274060	2	AC095184	AC095184 Rattus no
35	104	21.3	1671	10	HAMCAD	M31621 Syrian hams
36	92.8	19.0	64476	2	AC124292	AC124292 Homo sapi
37	92.8	19.0	159707	9	AC013403	AC013403 Homo sapi
38	90.2	18.4	123280	2	AC025662	AC025662 Homo sapi
39	86.4	17.7	2056	9	AF015947	AF015947 Homo sapi
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45	39	8.0	50	6	AX055746	AX055746 Sequence

ALIGNMENTS

RESULT 1  
BC057097 979 bp mRNA linear ROD 08-OCT-2003  
LOCUS Mus musculus cDNA clone MGC:61368 IMAGE:5714599, complete cds.  
DEFINITION BC057097  
ACCESSION BC057097.1 GI:34785321  
VERSION MGC.  
KEYWORDS Mus musculus (house mouse)  
SOURCE  
ORGANISM  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (Bases 1 to 979)  
REFERENCE  
AUTHORS  
Straussberg,R.L., Feingold,B.A., Grouse,L.H., Derge,J.G.,  
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,  
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,



**TITLE**  
JOURNAL

**REMARK**  
COMMENT

Direct Submission  
Submitted (31-MAR-2003) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabs@mail.nih.gov](mailto:cgabs@mail.nih.gov)  
Tissue procurement: Dr. Michael Brownstein  
cDNA Library Preparation: Michael Brownstein / Ted Uedin  
Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
[info@bcgsc.bc.ca](mailto:info@bcgsc.bc.ca)  
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,  
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,  
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo  
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven  
Nesse, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline  
Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Stott,  
Michael Thorne, Miranada Teai, Natasja van den Bosch, Jill Vardy,  
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL plate: 45 Row: d Column: 21  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Similarity but not  
identity to protein.  
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AS"

**ORIGIN**  
source  
Query Match 96.2%; Score 470.4; DB 10; Length 896;  
Best Local Similarity 99.2%; Pred. No. 4.4e-146;  
Matches 482; Conservative 0; Mismatches 13; Indels 1; Gaps 1;  
QY 5 GAGGCTAGATCTTCAGAACTGTTCCTG-AGGATCTGTGTCACAACTTTTACAGGCTTA 63  
Db 118 GAGGCTAGATCTTCAGAACTGTTCCTGAGGATCTGTGTCACAACTTTTACAGGCTTA 177  
QY 64 TACTGCTATTATCATAGACTTCAGGCAAACTCTCTCAAGGATGATTTGGCCAAACACCTT 123  
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QY 124 CCCTGGGTTTACTCAGCTGCAGACTCTGATCTACCAAGAGTGTTCCTGCTGGAGG 183  
Db 238 CCCTGGGTTTACTCAGCTGCAGACTCTGATCTACCAAGAGTGTTCCTGCTGGAGG 297  
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QY 304 TGACGGTCCCTGGTCTTTTTCAGTGCCTTTCGTGTGATGGTTTTCATGATACAAAGTGTAT 363  
Db 418 TGACGGTCCCTGGTCTTTTTCAGTGCCTTTCGTGTGATGGTTTTCATGATACAAAGTGTAT 477  
QY 364 GAGGACGGGCTCAATTTTCACTGCTTATGTTCCTTTGGGATTTCTGGATPCCACGCTAGC 423  
Db 478 GAGGACGGGCTCAATTTTCACTGCTTATGTTCCTTTGGGATTTCTGGATPCCACGCTAGC 537  
QY 424 CATCTNCAATCTACTTTTGGGACCCAGCCGCGGAAGCCAAAGCTTATGAGCCACACA 483  
Db 538 CATCTCAATTTTACTTTTGGGACCCAGCCGCGGAAGCCAAAGCTTATGAGCCACACA 597  
QY 484 AGACTT 489  
Db 598 AGACTT 603

**RESULT 3**  
BD076403  
LOCUS  
DEFINITION Human protein having transmembrane domain and DNA encoding the  
same.  
BD076403  
VERSION BD076403.1 GI:22622006  
KEYWORDS JP 2001519154-A/17.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 905)  
Kato, S., Kimura, T., Sekine, S. and Kobayashi, M.  
Human protein having transmembrane domain and DNA encoding the same  
Patent: JP 2001519154-A 17 23-OCT-2001;  
SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC  
COMMENT OS Homo sapiens (human)  
PN JP 2001519154-A/17  
PD 23-OCT-2001  
PF 05-OCT-1998 JP 2000515001  
PI SEISHI KATO, TOMOKO KIMURA, SHINGO SEKINE, MIDORI KOBAYASHI PC  
C12N15/09, C07K14/47, C12N5/10, C12N15/00, C12N5/00 CC Human protein  
having transmembrane domain  
and DNA encoding the  
same  
CC Key Location/Qualifiers  
FH source 1..905  
FT /organism="Homo sapiens (human)".  
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source  
1..905  
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/db\_xref="taxon:9606"

**ORIGIN**  
Query Match 72.2%; Score 353; DB 6; Length 905;  
Best Local Similarity 84.0%; Pred. No. 1.1e-106;  
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;  
QY 4 TGAGCTAGATCTTCAGAACTGTTCCTT-GAGGATCTGTGTCACAACTTTTACAGGCTT 62  
Db 226 TGGGCTGGATCTCCAGAACTGTTCCTGAGGAGCCCTGTGTCACAACTTTTACAGGCTT 285  
QY 63 ATACTGCTATTATCATAGACTTCAGGCAAACTCTCTCAAGGATGATTTGGCCAAACACCT 122  
Db 286 ATACCACTGCTATAGACTTCAGCAAAACCCCTTCAAGGATGATTTGGCCAAACACCT 345  
QY 123 TCCGTGGGTTTACTCAGCTGCAGACTCTGATCTACCAAGAGTGTTCCTGCTGGAG 182  
Db 346 TCCGTGGGTTTACTCAGCTGCAGACTCTGATCTACCAAGAGTGTTCCTGCTGGAG 405  
QY 183 GTAGTAATGCTGGGCAAACTTACTTCTTTCAAGGACAAAGCAGATTTGCCAAGGGCAAA 242





Db 584 TCGCGCAGGGCTCGTTCTCTCACTGCTATGTTCTTCGGGATTCCTGGAGCCACCTCTAT 643  
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QY 483 AAGACTT 489  
Db 704 AGGTCTT 710

RESULT 5  
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LOCUS  
DEFINITION  
Sequence 1 from Patent WO073348.  
ACCESSION  
AX055686  
VERSION  
AX055686.1 GI:12228826  
KEYWORDS  
Homo sapiens (human)  
SOURCE  
Homo sapiens  
ORGANISM  
Homo sapiens  
REFERENCE  
1  
AUTHORS  
Baker, K.P., Goddard, A., Gurney, A.L., Hebert, C., Henzel, W., Kabakoff, R.C., Shelton, D.L., Smith, V., Watanabe, C.K. and Wood, W.I.  
TITLE  
Methods and compositions for inhibiting neoplastic cell growth  
JOURNAL  
Patent: WO 0073348-A 1 07-DEC-2000;  
Genentech, Inc. (US)  
FEATURES  
source  
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Location/Qualifiers  
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Best Local Similarity 84.0%; Pred. No. 1.1e-106;  
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QY 4 TGAGGCTAGATCTTCAGACTGTTCCCT - GAGGATCTCGTCCAACTTTTACAGGCTT 62  
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QY 183 GTAGTAATGCTGGCAATGTTACTTCTTCAAGGCAAGACAGATTTGCCAAGGCAAA 242  
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Db 529 CTGATGGTCCAGGCTTTTTCAGTGGCTTTTTCAGTGGCTTTTTCATGGATACAAGTGA 588  
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Db 709 AGGTCTT 715

RESULT 6  
AX076904  
LOCUS  
DEFINITION  
Sequence 16 from Patent WO0105836.  
ACCESSION  
AX076904  
VERSION  
AX076904.1 GI:13121563  
KEYWORDS  
Homo sapiens (human)  
SOURCE  
Homo sapiens  
ORGANISM  
Homo sapiens  
REFERENCE  
1  
AUTHORS  
Botstein, D., Goddard, A., Gurney, A.L., Hillan, K.J., Roy, M.A. and Wood, W.I.  
TITLE  
Polypeptidic compositions and methods for the treatment of tumors  
JOURNAL  
Patent: WO 0105836-A 16 25-JAN-2001;  
Genentech, Inc. (US)  
FEATURES  
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Db 649 CCGTCTCCAATCTGCTTTCAGTGGGACCCAGCGCCGAAAGCCAAAGCTTATGACTACAT 708  
QY 483 AAGACTT 489  
Db 709 AGGTCTT 715

RESULT 7  
AX077021  
LOCUS  
DEFINITION  
Sequence 9 from Patent WO0105972.

ACCESSION AX077021  
VERSION AX077021.1 GI:13121656  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Ashkenazi, A.J., Baker, K.P., Pong, S., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Mark, M.R., Marsters, S.A., Pitti, R.M., Tumas, D., Watanabe, C.K. and Wood, W.I.  
TITLE Compositions and methods for the treatment of immune related diseases  
JOURNAL Patent: WO 0105972-A 9 25-JAN-2001;  
Genentech, Inc. (US)  
FEATURES source  
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ORIGIN  
Query Match 72.2%; Score 353; DB 6; Length 932;  
Best Local Similarity 84.0%; Pred. No. 1.1e-106;  
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;  
QY 4 TGAGGCTAGATCTTCAGAACTGTTCCTT-GAGGATCCTGCTCCAACTTTTACAGGCTT 62  
Db 229 TGGGCTGGATCTCCAGAACTGTTCCTTGGAGGACCTTGGTCCAACTTTTATCAGGCAC 288  
QY 63 ATACTGCTATTATCATAGACTTCAGGCAAACTCCTCTCAAGGATGATTTGGCCCAACCT 122  
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QY 183 GTAGTAATGCTGGGCAAACTTACTTCTTCAAGGCAAGCAAGATTTGCCAAGGGCAAA 242  
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Db 649 CCGTCTCCATTTCTGTTTGGGACCCAGCGCCGGAAGCCAGGCTTATGAGCCACAC 708  
QY 483 AAGACTT 489  
Db 709 AGGTCTT 715

RESULT 9  
AX358968  
LOCUS Homo sapiens clone DNA34387 APR--3 (UNQ214) mRNA, complete cds.  
DEFINITION Homo sapiens  
ACCESSION AX358968  
VERSION AX358968.1 GI:37183053  
KEYWORDS FLI\_CDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 932)  
AUTHORS Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, B., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E., Heidens, S., Huang, A., Kim, H.S., Klimowski, L., Jit, Y., Johnson, S.,

AX077021  
VERSION AX077021.1 GI:13121656  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Ashkenazi, A.J., Baker, K.P., Pong, S., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Mark, M.R., Marsters, S.A., Pitti, R.M., Tumas, D., Watanabe, C.K. and Wood, W.I.  
TITLE Compositions and methods for the treatment of immune related diseases  
JOURNAL Patent: WO 0105972-A 9 25-JAN-2001;  
Genentech, Inc. (US)  
FEATURES source  
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Location/Qualifiers  
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Best Local Similarity 84.0%; Pred. No. 1.1e-106;  
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;  
QY 4 TGAGGCTAGATCTTCAGAACTGTTCCTT-GAGGATCCTGCTCCAACTTTTACAGGCTT 62  
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Db 709 AGGTCTT 715

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ACCESSION AX574480  
VERSION AX574480.1 GI:27551793  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seehagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Watanabe, C., Watanabe, C., Watanabe, C., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I., and Godowski, P.

The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment

Genome Res. 13 (10), 2265-2270 (2003)

12975309

2 (bases 1 to 932)

Clark, H.F.

Direct Submission

Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA

Location/Qualifiers

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## TITLE

## JOURNAL

## PUBMED

## AUTHORS

## JOURNAL

## FEATURES

## source

## gene

## CDS

## ORIGIN

Query Match 72.2%; Score 353; DB 9; Length 932;  
Best Local Similarity 84.0%; Pred. No. 1.1e-106;  
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QY 4 TGAGGCTAGATCTTCAGACTGTTCCT-GAGATCTCTGTCACAACTTTTACAGGCTT 62  
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DB 709 AGGTCTT 715

## RESULT 10

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITILE

## JOURNAL

## MEDLINE

## PUBMED

## AUTHORS

## TITILE

## JOURNAL

## REMARK

## COMMENT

## FEATURES

## source

BC011006 940 bp mRNA linear PRI 12-NOV-2003  
Homo sapiens apoptosis related protein APR-3, transcript variant 2,  
mRNA (cDNA clone MGC:13322 IMAGE:4103408), complete cds.

BC011006

BC011006.1 GI:15029605

MGC

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 940)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

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Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

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Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., R.A.,

Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,

Schneerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 940)

Strausberg, R.

Direct Submission

Submitted (25-JUL-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: CLONTECH Laboratories, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

contact: [amadanes@systemsbio.org](mailto:amadanes@systemsbio.org)

Manup Madan, Jessica Fahney, Erin Helton, Mark Ketterman, Anuradha

Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 18105011.

Location/Qualifiers

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ORIGIN
Query Match 72.2%; Score 353; DB 9; Length 940;
Best Local Similarity 84.0%; Pred. No. 1.le-106;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

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ACCESSION BC035850
VERSION BC035850.1
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 970)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

```

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Klausner,R.D., Collins,P.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Shat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heien,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalios,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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2. (bases 1 to 970)
Direct Submission
Strausberg,R.
Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nih.gov
Ahter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Graniter,S., Guan,X., Gupta,J., Haghigati,F.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
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Young,A., Zhang,L.-H. and Green,E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 79 Row: n Column: 12
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 18105011.
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WATQRKAKTS"									
ORIGIN									
Query Match 72.2%; Score 353; DB 9; Length 970;									
Best Local Similarity 84.0%; Pred. No. 1.1e-106;									
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;									
QY	4	TCAGGCTAGATCTTCAGAACTGTTCCT-GAGGATCCTGGTCCAAACTTTTACAGGCTT	62						
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QY	63	ATATGCTATTATCATAGACCTTCAGCAAACTCTCAAGGATGATTTGGCCAACTCT	122						
DB	282	ATACCACTGTCTATAGACCTTCGAAGCAAAACCCCTCAAGGATGATTTGGCCAACTCT	341						
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BC021237									
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ACCESSION									
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
1 (bases 1 to 1056)									
REFERENCE									
AUTHORS									
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,									
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Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,									
TITLE									
JOURNAL									
MEDLINE									
PUBMED									
2 (bases 1 to 1056)									
Strausberg, R.									
Direct Submission									
Submitted (14-JAN-2002) National Institutes of Health, Mammalian									
Gene Collection (MGC), Cancer Genomics Office, National Cancer									
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,									
USA									
NIH-MGC Project URL: http://mgc.nci.nih.gov									
On Aug 20, 2003 this sequence version replaced gi:18204610.									
Contact: MGC help desk									
Email: cgapbs-r@mail.nih.gov									
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Clone distribution: MGC clone distribution information can be found									
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Series: IMAGE Plate: 26 Row: p Column: 21									
This clone was selected for full length sequencing because it									
passed the following selection criteria: matched mRNA gi: 18105011.									
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source									
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Best Local Similarity 84.0%; Pred. No. 1.1e-106;									
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;									



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QY 183 GTAGTAATCCCTGGGCAATGTTACTCTTCAAGGCAAGCAGATTTGCCAAGGGCAAA 242  
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QY 483 AAGACTT 489  
Db 1052 AGGTCTT 1058

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LOCUS Homo sapiens p18 protein (p18) mRNA, linear PRI 02-JUL-2001  
DEFINITION AF275744  
ACCESSION AF275744  
VERSION AF275744.1 GI:14582226  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Yang,Y.C., Chen,S.Y. and Chang,M.S.  
TITLE Cloning and characterization of p18  
JOURNAL Unpublished  
REFERENCE  
AUTHORS Yang,Y.C., Chen,S.Y. and Chang,M.S.  
TITLE Direct Submission  
JOURNAL Submitted (06-JUN-2000) Dept. of Medical Research, Mackey Memorial Hospital, 45 Minshen Rd., Tamsui, Taipei 251, Taiwan

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Best Local Similarity 83.8%; Pred. No. 3.9e-106;  
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QY 483 AAGACTT 489  
Db 710 AGGTCTT 716

Search completed: June 25, 2004, 22:57:48  
Job time : 2308 secs





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 20:25:07 ; Search time 725 Seconds  
(without alignments)

2865.336 Million cell updates/sec

Title: US-09-773-476-294

Perfect score: 489  
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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq 29Jan04:\*

- 1: Geneseqn1980as:\*
- 2: Geneseqn1990as:\*
- 3: Geneseqn2000as:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2003as:\*
- 8: Geneseqn2003bs:\*
- 9: Geneseqn2003cs:\*
- 10: Geneseqn2004as:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	353	72.2	905	2 AAX36813	Aax36813 Human tra
2	353	72.2	923	2 AAT85082	Aat85082 Transform
3	353	72.2	923	4 AAS08543	Aas08543 DNA encod
4	353	72.2	923	6 ABA92166	Abas92166 Human tra
5	353	72.2	932	2 AAX28432	Aax28432 EGF-like
6	353	72.2	932	3 AAC58584	Aac58584 Human PRO
7	353	72.2	932	3 AAA30036	Aaa30036 Human PRO
8	353	72.2	932	4 AAC91553	Aac91553 Human PRO
9	353	72.2	932	4 AAF30054	Aaf30054 Human CDN
10	353	72.2	932	4 AAF60356	Aaf60356 PRO240 co
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12	353	72.2	932	7 ACA57990	ACA57990 CDNA enco
13	353	72.2	932	8 ADA01275	Ada01275 Human PRO
14	353	72.2	932	8 ADA43704	Ada43704 Human CDN
15	353	72.2	932	8 ADA43472	Ada43472 Human CDN
16	353	72.2	932	8 ADA01147	Ada01147 Human PRO
17	353	72.2	932	8 ADA01031	Ada01031 Human CDN
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24 353 72.2 932 9 ADB99747 Adb99747 Human PRO  
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26 353 72.2 932 9 ADB65953 Adb65953 Human CDN  
27 353 72.2 932 9 ADC23351 Adc23351 Human CDN  
28 353 72.2 932 9 ADC26044 Adc26044 Human PRO  
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30 353 72.2 932 9 ADE11177 Ade11177 Human PRO  
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#### ALIGNMENTS

##### RESULT 1

AAX36813  
ID AAX36813 standard; DNA; 905 BP.

XX AC AAX36813;

XX DT 14-JUL-1999 (first entry)

XX DE Human transmembrane protein coding sequence, HP10435.

XX KW Transmembrane protein; human; cell membrane; proliferation; diagnosis;  
cell differentiation; carcinostatic agent; probe; gene therapy;  
XX KW signal transduction; apoptosis; inhibitor;  
XX KW phosphatidyethanolamine N-methyltransferase; ss.

XX OS Homo sapiens.

XX PN WO9918203-A2.

XX PD 15-APR-1999.

XX PF 05-OCT-1998; 98WO-JF004475.

XX PR 08-OCT-1997; 97JP-00276271.

XX PA (SAGA ) SAGAMI CHEM RES CENT.

XX PA (PROT-) PROTEGENE INC.

XX PI Kato S, Yamaguchi T, Sekine S, Kobayashi M;

XX DR WPI; 1999-277268/23.

XX DR P-PSDB; AAY13944.

XX PT Human transmembrane proteins and nucleotide sequences.

XX XX Claim 4; Page 125-126; 139pp; English.

XX CC This sequence encodes a human transmembrane protein of the invention. All  
of the proteins exist in the cell membrane, so are considered to be  
proteins controlling the proliferation and differentiation of the cells.  
XX CC They may be useful as carcinostatic agents or as antigens for preparing  
antibodies against the proteins. The cDNAs can be used as probes for gene  
diagnosis and gene sources for gene therapy, as well as for large-scale  
expression of the proteins. The HP01498 (see AAY13939) protein may be  
associated with signal transduction associated with apoptosis, and  
therefore useful in inhibition of apoptosis. The HP01962 (see AAY13943)

CC protein can be used to treat diseases associated with  
 CC phosphatidylethanolamine N-methyltransferase. The proteins are identified  
 CC by the presence of a hydrophobic transmembrane region, knowledge of the  
 CC protein function is not required, as in e.g. methods of expression  
 CC cloning  
 XX  
 SQ Sequence 905 BP; 218 A; 241 C; 211 G; 235 T; 0 U; 0 Other;

Query Match 72.2%; Score 353; DB 2; Length 905;  
 Best Local Similarity 84.0%; Pred. No. 3.3e-103;  
 Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;  
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 QY 483 AAGACTT 489  
 Db 706 AGGTCTT 712

RESULT 2  
 AAT85082  
 ID AAT85082 standard; DNA; 923 BP.  
 XX  
 AC AAT85082;  
 XX  
 DT 28-JAN-1998 (first entry)  
 XX  
 DE Transforming growth factor alpha HIII polynucleotide.  
 KW human transforming growth factor; TGF; TGF-alpha-HIII; angiogenesis;  
 KW embryogenesis; ocular disorder; kidney disorder; liver disorder;  
 KW alopecia; inflammation; ds.  
 XX Homo sapiens.

XX Key Location/Qualifiers  
 FH 5..691  
 CDS /\*tag= c  
 FT /\*product= "TGF-alpha-HIII"  
 FT 5..79  
 FT sig\_peptide /\*tag= a  
 FT 80..691  
 FT mat\_peptide /\*tag= b  
 FT

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 XX /product= "TGF-alpha-HIII"  
 PN WO9725349-Al.  
 XX 17-JUL-1997.  
 PD  
 XX 04-JAN-1996; 96WO-US000149.  
 XX  
 XX 04-JAN-1996; 96WO-US000149.  
 PR  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX Wei Y;  
 PI  
 XX WPI: 1997-372817/34.  
 DR P-PSDB; AAW27087.  
 DR  
 XX New human transforming growth factor-alpha homologue - used for  
 PT developing products for treating e.g. neurological disorders, kidney and  
 PT liver disorders, tumours, wounds, hair loss or skin disorders.  
 PT  
 XX Claim 7; Page 45-46; 63pp; English.  
 PS  
 XX This DNA sequence encodes a protein that has been putatively identified  
 CC as a human transforming growth factor (TGF) alpha analogue, TGF-alpha-  
 CC HIII. This protein can stimulate angiogenesis, embryogenesis, cell  
 CC differentiation and function. It can be used for therapeutic purposes for  
 CC restoration or enhancement of neurological functions diminished as a  
 CC result of trauma or other damaging pathologies such as AIDS dementia and  
 CC senile dementia, to treat ocular disorders, e.g. corneal inflammation, to  
 CC destroy target cells, to treat tumours, kidney or liver disorders or to  
 CC treat wounds, burns or ulcers. The polypeptide can also be used in the  
 CC modulation of angiogenesis, bone resorption, immune response, acid  
 CC synaptic and neuronal effector functions, or the arachidonic acid  
 CC cascade. It can also be used in applications related to terminal  
 CC differentiation e.g. in hyperproliferative disorders such as inflammation  
 CC or psoriasis and for alopecia, or other skin conditions which affect hair  
 CC follicular development. Antagonists to TGF-alpha-HIII can be used for  
 CC treating tumours or skin disorders such as psoriasis. The products can  
 CC also be used for diagnosis and detection of the above disorders  
 XX  
 SQ Sequence 923 BP; 235 A; 240 C; 210 G; 238 T; 0 U; 0 Other;

Query Match 72.2%; Score 353; DB 2; Length 923;  
 Best Local Similarity 84.0%; Pred. No. 3.4e-103;  
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 Db |||||  
 QY 282 ATACCACCTGTCTATAGACTGCAAGCAAAACCCCTCAAGGTGACTTTGCCCAACACCT 341  
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 QY 342 TCCGTGGCTTTACTCAGCTCCAGACTCTGATCTGCCCAACATGTCACATGCTCTGGAG 401  
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Db 582 TGGCCAGGCTGTTCTCACTGTTATGTTCTTGGGATTCGGAGCCACCACTCTAT 641  
QY 423 CCATCTNCATTTACTTTGGGAACCCAGCGCGGAAAGCCAAAGCTTATGAGCCAC 482  
Db 642 CCGTCTCCATTGCTTTGGGAGCCAGCGCGGAAAGCCAAAGCTTATGAGCTAT 701  
QY 483 AAGACTT 489  
Db 702 AGGTCTT 708

RESULT 3  
ID AAS08543 standard; cDNA; 923 BP.  
XX  
AC AAS08543;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE DNA encoding transforming growth factor (TGF) alpha HIII.  
XX  
KW Human; TGF alpha HIII; transforming growth factor alpha HIII; cancer;  
KW diagnostic; therapeutic; immune disorder; multiple sclerosis;  
KW systemic lupus erythematosus; human immuno-deficiency virus; HIV;  
KW hyperproliferative disorder; Gaucher's disease; cardiovascular disease;  
KW Schmitz syndrome; Chaga's cardiomyopathy; coronary arteriosclerosis;  
KW angiogenic disorder; corneal graft; neovascularisation; wound healing;  
KW diabetic retinopathy; neurological disorder; Huntington's chorea;  
KW Alzheimer's disease; Parkinson's disease; ss.  
XX  
OS Homo sapiens.

XX FH Key Location/Qualifiers  
XX CDS 5..694  
XX FT /\*tag= a  
XX FT /product= "TGF alpha HIII"  
XX FT /notes= "Transforming growth factor (TGF) alpha HIII"  
XX FT sig\_peptide 5..79  
XX FT /\*tag= b  
XX FT mat\_peptide 80..691  
XX FT /\*tag= c  
XX FT /note= "Mature TGF alpha HIII"  
XX PN WO200140251-A1.

XX  
XX 07-JUN-2001.  
XX  
XX 01-DEC-2000; 2000WO-US032745.  
XX  
XX 02-DEC-1999; 99US-0168387P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Wei Y;  
XX  
XX WPI; 2001-441480/47.  
XX P-PSDB; AAU04295.  
XX

PT Nucleic acid encoding human transforming growth factor alpha III (TGFA),  
PT useful for preventing, diagnosing and/or treating e.g. Cancer and  
PT Parkinson's disease.  
XX  
XX Claim 1; Fig 1; 302pp; English.  
XX

CC The sequence represents the coding sequence of human transforming growth  
CC factor (TGF) alpha HIII. TGF alpha HIII nucleic acid and protein may be  
CC used in the prevention, diagnosis and treatment of diseases associated  
CC with inappropriate polypeptide expression, for example immune disorders  
CC (e.g. multiple sclerosis, systemic lupus erythematosus and human immuno-  
CC deficiency virus (HIV) infections), hyperproliferative disorders (e.g.  
CC cancers and Gaucher's disease), cardiovascular diseases (e.g. Schmitz  
CC syndrome, Chaga's cardiomyopathy and coronary arteriosclerosis),  
CC angiogenic disorders (e.g. corneal graft neovascularisation and diabetic

CC retinopathy), neurological disorders (e.g. Huntington's chorea,  
CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or  
CC for promoting wound healing, regeneration and/or chemotaxis (full details  
CC given in specification). Additionally, the nucleic acid may be used to  
CC produce the secreted polypeptides, by inserting the nucleic acids into a  
CC host cell and culturing the cell to express the protein. It may also be  
CC used as a DNA probe in diagnostic assays to detect and quantitate the  
CC presence of similar nucleic acid sequences in samples, and therefore  
CC which patients may be in need of restorative therapy. The polypeptides  
CC may also be used as antigens in the production of antibodies against TGF  
CC alpha HIII and in assays to identify modulators of TGF alpha HIII. The  
CC anti-TGF alpha HIII antibodies may also be used as diagnostic agents for  
CC detecting the presence of TGF alpha HIII in samples (e.g. by enzyme  
CC linked immunosorbent assay (ELISA))  
XX  
SQ Sequence 923 BP; 235 A; 240 C; 210 G; 238 T; 0 U; 0 Other;  
Query Match 72.2%; Score 353; DB 4; Length 923;  
Best Local Similarity 84.0%; Pred. No. 3.4e-103;  
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;  
QY 4 TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCTGTTCCAACTTTTACAGGCTT 62  
Db 222 TGGGCTGGATCTCCAGAACTGTTCTCTGGAGACCTGTTCCAACTTTTATCAGGCAC 281  
QY 63 ATACTGCTATTATCATAGACCTTCAGCAAAATCCTCTCAAGGATGATTTGGCCAAACCT 122  
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Db 642 CCGTCTCAITTTCTGCTTTTGGGACCCAGCGCGGAAAGCCAAAGCTTATGAGCTAT 701  
QY 483 AAGACTT 489  
Db 702 AGGTCTT 708

RESULT 4  
ID ABA92166 standard; cDNA; 923 BP.  
XX  
AC ABA92166;  
XX  
DT 06-JUN-2002 (first entry)  
XX  
DE Human transforming growth factor alpha HIII cDNA.  
XX  
KW Transforming growth factor alpha HIII; TGF alpha HIII; human;  
KW antiinflammatory; anticancer; vulnery; ophthalmological;  
KW neuroprotective; antipsoriatic; gene therapy; diagnosis; gene; ss.  
XX  
OS Homo sapiens.

```

XX FH Key Location/Qualifiers
XX CDS 5..694 /*tag= a
XX FT /product= "TGF_alpha_HIII"
XX FT 5..79 /*tag= b
XX FT 80..691 /*tag= c
XX FT mat_peptide
XX FT sig_peptide
XX DN US2002025553-A1.
XX PD 28-FEB-2002.
XX XX 01-DEC-2000; 2000US-00726348.
XX PR 04-JAN-1996; 96US-0011136P.
XX PR 03-JAN-1997; 97US-00778545.
XX PR 02-DEC-1999; 99US-0168387P.
XX PA (WEIY/) WEI Y.
XX XX Wei Y;
XX PI WPI; 2002-280092/32.
XX DR P-PSDB; AAM51083.
XX XX Isolated nucleic acid molecule encoding Transforming Growth Factor alpha
XX PT HIII is used in preventing, treating or ameliorating a medical condition
XX PT e.g. cardiovascular or autoimmune diseases.
XX XX Claim 1; Fig 1A-B; 118pp; English.
XX CC The present sequence is that of cDNA (ATCC 97342) encoding human
XX CC transforming growth factor alpha HIII (TGF alpha HIII, see AAM51083), a
XX CC novel member of the TGF family. The cDNA was discovered in a human testis
XX CC cDNA library. The invention provides TGF alpha HIII nucleic acid
XX CC molecules (including those comprising sequential deletions from either
XX CC end of the present sequence) and polypeptides, vectors, host cells,
XX CC antibodies and recombinant methods for producing the polypeptides. The
XX CC TGF alpha HIII polypeptides and polynucleotides can be used in diagnostic
XX CC methods for detecting disorders related to TGF alpha HIII, and also for
XX CC therapeutic purposes, e.g. to stimulate wound healing to restore normal
XX CC neurological functioning after trauma or AIDS dementia, to treat ocular
XX CC disorders, to target certain cells, to treat kidney and liver disorders,
XX CC to promote hair follicular development, to stimulate angiogenesis for the
XX CC treatment of burns, ulcers and corneal incisions, and to stimulate
XX CC embryogenesis. Autoimmune diseases, disorders of haematopoietic cells,
XX CC allergic reactions, cardiovascular diseases, organ rejection,
XX CC inflammation, and hyperproliferative disorders may also be treated e.g.
XX CC by gene therapy. Methods are also provided for identifying agonists and
XX CC antagonists of TGF alpha HIII. Antagonists may be used to inhibit the
XX CC action of TGF alpha HIII polypeptides in the treatment of corneal
XX CC inflammation, neoplasia such as tumours and cancers, and psoriasis
XX SQ Sequence 923 BP; 235 A; 240 C; 210 G; 238 T; 0 U; 0 Other;
XX
Query Match 72.2%; Score 353; DB 6; Length 923;
Best Local Similarity 84.0%; Pred No. 3.4e-103;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;
XX 4 TGAGGCTAGATCTTCAGAACTGTTCCCT-CAGGATCTCTGTCACAACTTTTACAGGCTT 62
XX 222 TGGGGCTGGATCTCCAGAACTGTTCTCTGAGGACCCCTGTCACAACTTTTCATCAGGCAC 281
XX 63 ATACTGTATATCATAGACTTCAGCAATCTCTCAGGATGATTTGGCCAAACACCT 122
XX 282 ATACCACTGTATCATAGACTGCAAGCAACCCCTCAAGGTGATCTTGCCCAACACCT 341
XX 123 TCCGTGGGTTTACTCAGCTCAGACTCTGATACCTACCAAGATGTTCCCTGTCCTGGAG 182
XX 342 TCCGTGGCTTTACTCAGCTCAGACTCTGATACCTGATCTGACCAACATGTCACACTGCTCGGAG 401

```

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QY 183 GTAGTAATGCTCTGGGACAAATCTTACTTTTTCATAGGACAAAGCAGATTTGCCAAGGCAAA 242
DB 402 GAAATTAATGCTGGGAATACTATACCTCTTATATAGACAAACAAATCTGTCAAGGGCAAA 461
QY 243 GGGACCTTTGCAANTAGCACTGGAAGCCCGAGAAATGTCTCTGAGAACGGATCTTTGTGCAT 302
DB 462 AGAACCTTTTGAATAACACACTGGGAGCCAGAAATGTCTCTGAGAAATGGATCTTTGTGTAC 521
QY 303 CTGACGGTCTCTGGTCTTTTTCAGTCCGTTTGTGTGATGTTTCCATGGATACAAAGTGTGA 362
DB 522 CTGATGGTCCAGGCTTTTTCAGTGTGTTTGTGTGATGTTTCCATGGATACAAAGTGTGA 581
QY 363 TGAGGCAGGGCTCATTTTCACTGCTTATATGTTCTTTGGATCTCGGATCCACACGCTAG 422
DB 582 TGCGCCAGGGCTCGTCTCTCACTGCTTATGTTCTTTGGGATCTCGGAGCCACCACTCTAT 641
QY 423 CCATCTNCATTTCTACTTTTGGGGAACCCAGAGCCCGGAAAGCCAAAGCTTATGAGCCACAC 482
DB 642 CGGTCTCCATTTCTGCTTTGGCGAGCCAGCCAGCCGAGCCGAGCCAAAGACTTCATGNACTACAT 701
QY 483 AAGACTT 489
DB 702 AGGTCTT 708
XX
RESULT 5
AAX28432
ID AAX28432 standard; DNA; 932 BP.
XX AC AAX28432;
XX DT 22-JUN-1999 (first entry)
XX DE EGF-like homologue PRO240 coding sequence.
XX KW Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246;
XX KW EBAF-2; inhibitor; tumour growth; cancer; EGF-like homologue;
XX KW FGF-8 homologue; ss.
XX OS Homo sapiens.
XX PN WO9914327-A2.
XX PD 25-MAR-1999.
XX PF 10-SEP-1998; 98WO-US018824.
XX PR 17-SEP-1997; 97US-0059114P.
XX PR 17-SEP-1997; 97US-0059117P.
XX PR 18-SEP-1997; 97US-0059263P.
XX PR 15-OCT-1997; 97US-0062125P.
XX PR 17-OCT-1997; 97US-0062285P.
XX PR 17-OCT-1997; 97US-0062287P.
XX PR 24-OCT-1997; 97US-0062816P.
XX PR 29-OCT-1997; 97US-0063704P.
XX PR 25-NOV-1997; 97US-0066840P.
XX (GETH ) GENENTECH INC.
XX Botstein D, Goddard A, Gurney A, Hillan K, Lawrence DA, Roy M;
XX Wood WI;
XX WPI; 1999-229532/19.
XX DR P-PSDB; AAY05282.
XX XX Antibodies against specific proteins overexpressed in tumors.
XX PT Example 1; Fig 11; 130pp; English.
XX CC This sequence encodes the EGF-like homologue PRO240. The invention
XX CC relates to antibodies (Ab) that bind to any of the polypeptides (I)
XX CC designated PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246
XX CC or EBAF-2. The Ab, or other agents that inhibit expression and/or

```

CC activity of (I) are used: (i) to inhibit growth of tumours; and (ii) as  
CC diagnostic/prognostic reagents for detection or quantification of (i) in  
CC cells or tissues, by standard immunoassays, with overexpression being  
CC indicative of cancer. For therapeutic use, the Ab may be conjugated to a  
CC toxin, chemotherapeutic agent or radioisotope. Genes expressing (I), many  
CC of which are growth factor homologues, are overexpressed in some cases of  
CC cancer

XX  
XX  
SQ Sequence 932 BP; 239 A; 241 C; 212 G; 237 T; 0 U; 3 Other;

Query Match 72.2%; Score 353; DB 2; Length 932;

Best Local Similarity 84.0%; Pred. No. 3.4e-103;  
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

QY 4 TGAGGCTAGACTTTCAGACTTTCCTTCCCTGAGATCCCTGCTCAAACTTTTACAGGCTT 62

Db 229 TGGGGCTGAGTCTCCAGAACTGTTCTGAGAGCCCTGGTCCAACTTTCATCAGGCAC 288

QY 63 ATACTGCTATTATCATAGACTTTCAGGCAAACTCTCTCAAGGATGATTGGCCACACCT 122

Db 289 ATACCACCTCATATAGACTTTCAGGCAAACTCTCTCAAGGATGATTGGCCACACCT 348

QY 123 TCGTGGGTTTACTGAGCTGAGACTCTGATACCTACCAAGATGTTCCCTGCTCTGGAG 182

Db 349 TCGTGGGTTTACTGAGCTTCCAGACTCTGATACCTACCAAGATGTTCCCTGCTGGAG 408

QY 183 GTAGTAATCCCTGGGCAATGTTACTTCTTCAAGGCAAGCAGATTTGCCAAGGGCAA 242

Db 409 GAATTAATCCCTGGGCAATGTTACTTCTTCAAGGCAAGCAGATTTGCCAAGGGCAA 468

QY 243 GGGACCTTTGCAATAGCACTGGAAGCCCAAGAAATGTCTGAGAACCGATCTTGTGAT 302

Db 469 AGAACCTTTGCAATAGCACTGGAAGCCCAAGAAATGTCTGAGAACCGATCTTGTGAT 528

QY 303 CTGAGCGTCTGCTTTTTCAGTGGTGTGCTGATGTTTCCATGGATACAGTCTGA 362

Db 529 CTGAGTCTGCTTTTTCAGTGGTGTGCTGATGTTTCCATGGATACAGTCTGA 588

QY 363 TGAGGCGAGGCTCAITTTTCACTGCTATGTTCTTTGGGATCTGGGATCCACCGCTAG 422

Db 589 TCGCGCAGGCTGCTTCTCACTGCTATGTTCTTTGGGATCTGGGATCCACCTCTAT 648

QY 423 CCATCTGCTTACTTTTGGGAACCCAGCGCGGGAAGCAAGCTTATGAGCCACAC 482

Db 649 CCGTCTCCATCTGCTTTGGGCGACCCAGCGCGGGAAGCAAGCTTATGAGCCACAC 708

QY 483 AAGACTT 489

Db 709 AGTCTT 715

## RESULT 6

AAC58584

ID AAC58584 standard; cDNA; 932 BP.

XX AAC58584;

AC AAC58584;

XX AAC58584;

DT 29-JAN-2001 (first entry)

XX Human PRO240 protein UNQ214 encoding cDNA SEQ ID NO:25.

XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
XX dermatological; antiarthritic; antirheumatic; immunosuppressive;  
XX haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;  
XX antianaemic; hepatotropic; viricide; antipsoriatic; anti allergic;  
XX antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
XX osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;  
XX idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
XX autoimmune vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
XX autoimmune thrombocytopenia; immune-mediated renal disease;  
XX demyelinating disease; hepatobiliary disease; Whipple's disease;  
XX inflammatory bowel disease; gluten-sensitive enteropathy;  
XX autoimmune disease; immune-mediated skin disease; allergic disease;

KW immunological disease; transplantation associated disease;  
KW graft rejection; graft-versus-host-disease; ss.

XX Homo sapiens.

XX WO2000053758-A2.

XX 14-SEP-2000.

XX 02-MAR-2000; 2000WO-US005841.

XX 08-MAR-1999; 99WO-US005028.

XX 10-MAR-1999; 99US-0123618P.

XX 12-MAR-1999; 99US-0123957P.

XX 23-MAR-1999; 99US-0125775P.

XX 12-APR-1999; 99US-0128849P.

XX 28-APR-1999; 99WO-US0008615.

XX 28-APR-1999; 99US-0132371P.

XX 14-MAY-1999; 99US-0134287P.

XX 02-JUN-1999; 99WO-US012252.

XX 23-JUN-1999; 99US-0141037P.

XX 20-JUL-1999; 99US-0144758P.

XX 26-JUL-1999; 99US-0145698P.

XX 28-JUL-1999; 99US-0146222P.

XX 01-SEP-1999; 99WO-US020111.

XX 08-SEP-1999; 99WO-US020594.

XX 13-SEP-1999; 99WO-US020944.

XX 15-SEP-1999; 99WO-US021090.

XX 15-SEP-1999; 99WO-US021547.

XX 05-OCT-1999; 99WO-US023089.

XX 29-OCT-1999; 99US-0162506P.

XX 29-NOV-1999; 99WO-US028214.

XX 30-NOV-1999; 99WO-US028313.

XX 30-NOV-1999; 99WO-US028409.

XX 01-DEC-1999; 99WO-US028301.

XX 02-DEC-1999; 99WO-US028634.

XX 02-DEC-1999; 99WO-US028551.

XX 02-DEC-1999; 99WO-US028564.

XX 16-DEC-1999; 99WO-US028565.

XX 16-DEC-1999; 99WO-US030095.

XX 20-DEC-1999; 99WO-US030999.

XX 30-DEC-1999; 99WO-US031274.

XX 05-JAN-2000; 2000WO-US000219.

XX 06-JAN-2000; 2000WO-US000376.

XX 11-FEB-2000; 2000WO-US003565.

XX 18-FEB-2000; 2000WO-US004341.

XX 18-FEB-2000; 2000WO-US004342.

XX 22-FEB-2000; 2000WO-US004414.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;

XX Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;

XX Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

XX WPI; 2000-572271/53.

XX P-PSDB; AAB33419.

XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of

XX immune related disorders, e.g. systemic lupus erythematosus, rheumatoid

XX arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

XX Claim 23; Fig 11; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can

XX be used in the treatment of immune related diseases. The human PRO

XX proteins, anti-PRO antibodies, agonists and antagonists are useful for

XX treating and diagnosing immune related disorders. The disorders are

XX selected from systemic lupus erythematosus, rheumatoid arthritis,

XX osteoarthritis, juvenile chronic arthritis, spondyloarthritis,

XX systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's

CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central and  
 CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel  
 CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune  
 CC or immune-mediated skin diseases, allergic diseases, immunological  
 CC diseases of the lung, and transplantation associated diseases including  
 CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58378  
 CC represent PCR primers and hybridisation probes used in the isolation of  
 CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477  
 CC represent human PRO polynucleotide and protein sequences given in the  
 CC exemplification of the present invention  
 XX  
 XX  
 SQ Sequence 932 BP; 239 A; 241 C; 214 G; 237 T; 0 U; 1 Other;  
 Query Match 72.2%; Score 353; DB 3; Length 932;  
 Best Local Similarity 84.0%; Pred. No. 3.4e-103;  
 Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;  
 QY 4 TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCCTGTCACAACTTTTACAGGCTT 62  
 DB 229 TGGGCTGGATCTCCAGAACTGTTCTCTGGAGACCTGTGTCACAACTTTTCATCAGGCAC 288  
 QY 63 ATACTGCTATTATCATAGACCTTCAGGCAAAATCCTCTCAAGGATGATTTGGCCAAACCTT 122  
 DB 289 ATACCCTGTCTATCATAGACCTGCAAGCAAAACCCCTCAAGGTGACTTGGCCAAACCTT 348  
 QY 123 TCCGTGGTGTACTCAGCTCAGACCTGATCTACTACCAAGATGTTCCCTGCTGGAG 182  
 DB 349 TCCGTGGCTTTACTCAGCTCCAGACTGTGATCTGACCAACATGCAACTGTCCTGGAG 408  
 QY 183 GTAGTATGCTCTGGGCAAAATCTTCTTTCAGGCAACAGCAGATTTGCCAAGGGCAAA 242  
 DB 409 GAAATTAATGCTGGAATACTATCACCCTTATATAGACACCAAAATCTGTCAAGGGCAAA 468  
 QY 243 GGGACCTTTGCAATAGCACTGGAGCCAGAAATGTCTCTGAGAACGGATCTTGTGCAT 302  
 DB 469 AGAACCTTTGCAATAGCACTGGAGCCAGAAATGTCTCTGAGAACGGATCTTGTGCAT 528  
 QY 303 CTGACGCTCTGGTCTTTTTCAGTGCCTTTTGTGATGTTTCCATGGATACAAAGTGA 362  
 DB 529 CTGATGCTCAGGCTCTTTTTCAGTGTGTTTGTGCTGATGTTTCCATGGATACAAAGTGA 588  
 QY 589 TGGCCAGGCTGCTTCTCACTGCTTATGTTCTTGGGATCTTGGAGCCACCACTCTAT 648  
 QY 423 CCATCTNCATCTACTTTGGGAAACCCAGCGCCGGAAGCCAGGCTTATGAGCCACAC 482  
 DB 649 CCGTCTCCATCTGCTTTGGGGACCCAGCGCCGGAAGCCAGGCTTATGAGCCACAC 708  
 QY 483 AAGACTT 489  
 DB 709 AGGTCTT 715

## RESULT 7

AAA30036

ID AAA30036 standard; cDNA; 932 BP.

XX AC

XX AC

XX AAA30036;

XX XX

DT 09-AUG-2000 (first entry)

XX XX

DE Human PRO240 nucleotide sequence.

XX XX

KW Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246;

KW PRO317; tumour growth inhibitor; cancer; diagnosis; treatment; human;

KW cell growth; proliferation; serrate precursor; C-serrate-1; ADEPT;

KW antibody dependent enzyme mediated prodrug therapy; chromosome 2; ss.

XX CS

CS Homo sapiens.

XX DB

PN WO200015666-A2.  
 XX 23-MAR-2000.  
 XX 08-SEP-1999; 99WO-US020594.  
 XX 10-SEP-1998; 98US-0099803P.  
 XX 10-SEP-1998; 98WO-US018824.  
 XX (GETH ) GENENTECH INC.  
 XX Goddard A, Gurney AL, Hallan KJ, Roy MA, Wood WI, Botstein D;  
 PI  
 XX WPI: 2000-271386/23.  
 DR P-PSDB; AAY88569.  
 XX  
 XX New isolated antibodies which bind to specific polypeptides used for  
 PT diagnosis and treatment of neoplastic cell growth and proliferation.  
 XX  
 XX Example 4; Fig 7; 200pp; English.  
 PS  
 CC This sequence represents a human PRO240 nucleotide sequence. PRO240  
 CC shares sequence homology with the D. melanogaster serrate precursor  
 CC protein and the Gallus gallus C-serrate-1 protein. The PRO240 gene is  
 CC located on chromosome 2. The invention relates to isolated antibodies  
 CC which bind to a polypeptide. The "PRO" polypeptides are encoded by genes  
 CC which are over expressed in the genome of tumour cells. Vectors and host  
 CC cells comprising the nucleic acid encoding the antibodies are used in the  
 CC production of the antibodies. The antibodies and nucleic acids encoding  
 CC them are used for diagnosing a tumour in a mammal. The antibodies are  
 CC used for inhibiting the growth of tumour cells and identifying compounds  
 CC that inhibit a biological or immunological activity of and/or expression  
 CC of a PRO187, PRO533, PRO214, PRO240, PRO211, PRO230, PRO261, PRO246 or  
 CC PRO317 polypeptide. The antibody can be used in antibody dependent enzyme  
 CC mediated prodrug therapy (ADEPT) by conjugating the antibody to a prodrug  
 CC -activating enzyme which converts a prodrug to an anti-cancer drug. The  
 CC antibodies can be fluorescently labelled and monitored by light  
 CC microscopy, flow cytometry or fluorimetry for diagnosis and prognosis of  
 CC tumours  
 XX  
 SQ Sequence 932 BP; 239 A; 241 C; 214 G; 237 T; 0 U; 1 Other;

## Query Match

72.2%; Score 353; DB 3; Length 932;

Best Local Similarity 84.0%; Pred. No. 3.4e-103;

Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

QY

4 TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCCTGTCACAACTTTTACAGGCTT 62

DB

229 TGGGCTGGATCTCCAGAACTGTTCTCTGGAGACCTGTGTCACAACTTTTCATCAGGCAC 288

QY

63 ATACTGCTATTATCATAGACCTTCAGGCAAAATCTCTCAAGGATGATTTGGCCAAACCTT 122

DB

289 ATACCCTGTCTATCATAGACCTGCAAGCAAAACCCCTCAAGGTGACTTGGCCAAACCTT 348

QY

123 TCCGTGGTGTACTCAGCTCAGACCTGATCTACTACCAAGATGTTCCCTGCTGGAG 182

DB

349 TCCGTGGCTTTACTCAGCTCCAGACTGTGATCTGACCAACATGCAACTGTCCTGGAG 408

QY

183 GTAGTATGCTCTGGGCAAAATCTTCTTTCAGGCAACAGCAGATTTGCCAAGGGCAAA 242

DB

409 GAAATTAATGCTGGAATACTATCACCCTTATATAGACACCAAAATCTGTCAAGGGCAAA 468

QY

243 GGGACCTTTGCAATAGCACTGGAGCCAGAAATGTCTCTGAGAACGGATCTTGTGCAT 302

DB

469 AGAACCTTTGCAATAGCACTGGAGCCAGAAATGTCTCTGAGAACGGATCTTGTGCAT 528

QY

303 CTGACGCTCTGGTCTTTTTCAGTGCCTTTTGTGATGTTTCCATGGATACAAAGTGA 362

DB

529 CTGATGCTCAGGCTCTTTTTCAGTGTGTTTGTGCTGATGTTTCCATGGATACAAAGTGA 588

QY

363 CTGACGAGGCTCATTTTCACTGCTTATGTTCTTGGGATCTTGGATCCACACGCTAG 422

DB

589 TGGCCAGGCTGCTTCTCACTGCTTATGTTCTTGGGATCTTGGAGCCACCACTCTAT 648

QY 423 CCATCTNCATCTTCTTCTTGGGAAACCCAGCGCGGAAAGCCAGGCTTATGAGCCAC 482  
DB 649 CGGTCTCCATCTTCTTCTTGGGCGACCCAGCGCGGAAAGCCAGGCTTATGAGCCAC 708  
QY 483 AAGACTT 489  
DB 709 AGGTCTT 715

RESULT 8  
AAC91553  
ID AAC91553 standard; cDNA; 932 BP.  
XX  
AC AAC91553;  
XX  
DT 21-MAR-2001 (first entry)  
XX  
DE Human PRO240 cDNA.  
XX  
KW Human; PRO; cytostatic; neurotropic; neuroprotective; respiratory general;  
KW antinflammatory; angiogenic; immunosuppressive; immunostimulant;  
KW PRO agonist; cancer; inflammatory disorder; immunological disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200073348-A2.  
XX  
PD 07-DEC-2000.  
XX  
PF 30-MAY-2000; 2000WO-US014941.  
XX  
PR 02-JUN-1999; 99WO-US012252.  
PR 22-JUN-1999; 99US-0140650P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 09-DEC-1999; 99US-0170262P.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030309.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US000356.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 03-MAR-2000; 2000US-0187202P.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;  
PI Shelton DL, Smith V, Watanabe CK, Wood WI;  
XX  
XX WPI; 2001-016509/02.  
DR P-PSDB; AAB50951.  
XX  
XX Twenty eight nucleic acids encoding PRO polypeptides which are useful for  
PT treating various tumors, e.g. breast cancer, and other inflammatory,  
PT angiogenic and immunological disorders.  
XX  
XX Claim 20; Fig 1; 188pp; English.  
XX  
XX The present sequence is one of twenty eight nucleic acids encoding PRO  
CC polypeptides. The PRO polypeptides and their agonists, including  
CC antibodies, peptides, and small molecule agonists, may be used to treat

CC various tumors, e.g., cancers such as breast cancer, ovarian cancer,  
CC renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung  
CC cancer, bladder cancer, central nervous system cancer, melanoma or  
CC leukemia. They are also useful for treating other disorders such as  
CC neuronal, glial, astrocytal, hypothalamic and other glandular  
CC macrophagal, epithelial, stromal and blastocoeleic disorders, and  
CC inflammatory, angiogenic and immunological disorders  
XX  
SQ Sequence 932 BP; 239 A; 241 C; 214 G; 237 T; 0 U; 1 Other;  
Query Match 72.2%; Score 353; DB 4; Length 932;  
Best Local Similarity 84.0%; Pred. No. 3.4e-103;  
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;  
QY 4 TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCTCTGTCACAACTTTTACAGGCTT 62  
DB 229 TGGGCTGGATCTCCAGAACTGTTCTCTGGAGACCTGCTGCCAACTTTCATCAGGCAC 288  
QY 63 ATACTGCTATTATCATAGACTTCAGGCAATCTCTCAAGGATGATTTGCCCAACACCT 122  
DB 289 ATACCATGTCTCATAGACTCTGCAAGCAACCCCTCAAAGTGACTTGGCCAAACCT 348  
QY 123 TCCGTGGGTTTACTCAGCTGCAGACTCTGATCTTACCACAAAGATGTTCCCTGTCTGGAG 182  
DB 349 TCCGTGGCTTTACTCAGCTCCAGACTCTGATCTGCCCAACATGTCAACTGTCTGGAG 408  
QY 183 GTAGTAATGCTGGGCAATGTTACTTCTTCAAGGACAGCAGATTTGCCAGGGGAAA 242  
DB 409 GAATTAATGCTGGAATACTATCACTCTTATATAGACAAACCAAACTGTCAAGGGGAAA 468  
QY 243 GGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTCTCTGAGAACGGATCTTGTGCAT 302  
DB 469 AGAACCTTTGCAATAACACTGGGACCCAGAAATGTCTCTGAGATGGATCTTGTGTAC 528  
QY 303 CTGACGGTCTGGTCTTTTTCAGTGGCTTTGCTGTGATGTTTCCATGGATAGAAAGTGA 362  
DB 529 CTGATGCTCCAGGTCTTTTTCAGTGGTGTGCTGTGATGTTTCCATGGATAGAAAGTGA 588  
QY 363 TGAGGACAGGCTCATTTTCACTGCTTATGTTTGGGATCTGGGATCCACACGCTAG 422  
DB 589 TGGCCAGGGCTGTTCTCACTGCTTATGTTTGGGATCTGGGATCTGGGACCCACTCTAT 648  
QY 423 CCATCTNCATCTTCTTGGGAAACCCAGCGCGGAAAGCCAGGCTTATGAGCCAC 482  
DB 649 CCGTCTCCATCTTCTTGGGCGACCCAGCGCGGAAAGCCAGGCTTATGAGCTACAT 708  
QY 483 AAGACTT 489  
DB 709 AGGTCTT 715

RESULT 9  
AAF30054  
ID AAF30054 standard; cDNA; 932 BP.  
XX  
AC AAF30054;  
XX  
XX 30-APR-2001 (first entry)  
XX  
XX Human cDNA encoding PRO240.  
XX  
KW PRO240; UNQ214; human; immune disease; autoimmune disease; antirheumatic;  
KW antiarthritic; antinflammatory; antianaemic; immunosuppressive;  
KW antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide;  
KW dermatological; antipsoriatic; antiasthmatic; antiallergic;  
KW immunostimulant; serrate; lung cancer; ss.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH 12..701  
CDS /\*tag= a  
FT sig\_peptide 12..101





PT useful for diagnosing and treating cancers.  
PS Claim 50; Fig 7; 196pp; English.  
XX  
CC The present invention relates to PRO proteins and coding sequences. The  
CC present sequence is the coding sequence for one such PRO protein. It was  
CC found that the PRO genes are amplified in the genome of tumour cells. The  
CC gene amplification is expected to be associated with the overexpression  
CC of the gene product and contributes to tumourigenesis. Therefore,  
CC antagonists of PRO proteins are useful for the treatment of benign or  
CC malignant tumours, leukaemias, lymphoid malignancies and other disorders  
CC such as neuronal, gliial, astrocytal, hypothalamic, glandular, epithelial,  
CC inflammatory and immunologic disorders  
XX  
SQ Sequence 932 BP; 239 A; 241 C; 214 G; 237 T; 0 U; 1 Other;  
Query Match 72.2%; Score 353; DB 4; Length 932;  
Best Local Similarity 84.0%; Pred. No. 3.4e-103;  
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;  
QY 4 TGAGGCTAGATCTTCAGAACTGTCCTTCTGGAGGACCTGGTCCAACTTTCATCAGGCAC 62  
Db 229 TGGGGCTGAGTCTCCAGAACTGTCCTTCTGGAGGACCTGGTCCAACTTTCATCAGGCAC 288  
QY 63 ATACTGCTATTATCATAGACCTTCAGGCAAACTCTCTCAGGATGATTTGGCCACACCT 122  
Db 289 ATACCACTGTCATCATAGACCTTCAGGCAAACTCTCTCAGGATGATTTGGCCACACCT 348  
QY 123 TCCGTGGGTTTACTCAGCTGCAGACTCTGATACCTACCAAGATGTCCTGCTCGGAG 182  
Db 349 TCCGTGGGTTTACTCAGCTGCAGACTCTGATACCTACCAAGATGTCCTGCTCGGAG 408  
QY 183 GTAGTAATCCCTGGGCAATGTTACTCTTTTCAAGCAAGCAGATTTGCCAAGGGCAAA 242  
Db 409 GAATTAATCCCTGGGCAATGTTACTCTTTTCAAGCAAGCAGATTTGCCAAGGGCAAA 468  
QY 243 GGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTCCTGAGAACGATCTTGTGCAT 302  
Db 469 AGAACCTTTGCAATAGCACTGGAAGCCAGAAATGTCCTGAGAACGATCTTGTGCAT 528  
QY 303 CTGACGGTCTCGTCTTTTSCAGTGGTGTGCTGATGTTTCCATGATACCAAGTGTGA 362  
Db 529 CTGATGGTCCAGTCTTTTSCAGTGGTGTGCTGATGTTTCCATGATACCAAGTGTGA 588  
QY 363 TGAGGAGGGCTCATTTTCACTGCTATGTTCTTTGGGATCTGGGATCCACACGCTAG 422  
Db 589 TCGGCCAGGGCTCGTTCTCACTGCTATGTTCTTTGGGATCTGGGATCCACACGCTAT 648  
QY 423 CCATCTNCAATCTTACTTTGGGAAACCCAGCGCGGAAAGCCCAAGGCTTTCATGAGCCAC 482  
Db 649 CCGTCTCGATTTGCTTTGGGACCCAGCGCGGAAAGCCCAAGGCTTTCATGAGCCAC 708  
QY 483 AAGACTT 489  
Db 709 AGTCTT 715  
RESULT 11  
ID ABK69964 standard; DNA; 932 BP.  
XX  
AC ABK69964;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE cDNA encoding human Pro peptide #4.  
XX  
KW Human; ss; gene; PRO; secreted protein; transmembrane protein;  
KW genetic disorder; tumour; cancer.  
XX  
OS Homo sapiens.  
XX  
PN W0200224888-A2.

XX  
PD 28-MAR-2002.  
XX  
PF 29-AUG-2001; 2001WO-US027099.  
XX  
XX 01-SEP-2000; 2000US-0229896P.  
PR 02-SEP-2000; 2000US-0230621P.  
PR 22-SEP-2000; 2000US-0235147P.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 12-JAN-2001; 2001US-0261878P.  
PR 16-JAN-2001; 2001US-0261910P.  
PR 16-JAN-2001; 2001US-0261939P.  
PR 16-JAN-2001; 2001US-0262150P.  
PR 25-JAN-2001; 2001US-0264395P.  
PR 02-FEB-2001; 2001US-0266421P.  
PR 28-FEB-2001; 2001US-0267623P.  
PR 09-MAR-2001; 2001WO-US006520.  
PR 03-APR-2001; 2001US-0280982P.  
PR 04-APR-2001; 2001US-0282129P.  
PR 04-APR-2001; 2001US-0282199P.  
PR 25-MAY-2001; 2001US-0290589P.  
PR 01-JUN-2001; 2001WO-US017092.  
PR 20-JUN-2001; 2001WO-US017800.  
PR 29-JUN-2001; 2001WO-US019692.  
PR 09-JUL-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
XX (GETH ) GENENTECH INC.  
PA Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,  
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z,  
PI Fong S;  
XX WPI; 2002-362426/39.  
DR P-PSDB; ABG34033.  
XX  
XX New PRO polypeptides and polynucleotides encoding the polypeptides,  
PT useful in gene therapy, chromosome identification, tissue typing, or for  
PT genetic analysis of individuals with genetic disorders.  
XX Claim 2; Fig 7; 219pp; English.  
XX This invention relates to the cDNA and protein sequences of novel  
CC secreted and transmembrane polypeptides PRO polypeptides. The invention  
CC also comprises a method for producing the proteins of the invention by  
CC recombinant means and antibodies specific for the protein of the  
CC invention. The antibody may be used for detecting the PRO proteins of the  
CC invention and may be used to modify their activity. polynucleotides may  
CC be used as hybridisation probes for a cDNA library to isolate the full-  
CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation  
CC probes for mapping the gene which encodes that PRO and for genetic  
CC analysis of individuals with genetic disorders, in assays to identify  
CC other proteins or molecules involved in binding reaction, to generate  
CC transgenic animals or knock-out animals which in turn are useful in the  
CC development and screening of therapeutically useful reagents, for  
CC chromosome identification, and tissue typing. The PRO polypeptides are  
CC useful in gene therapy, and as molecular weight markers for protein  
CC electrophoresis purposes. The sequences may also be used to detect  
CC overexpression on PRO polypeptides in cancerous tumours and for screening  
CC for differentially expressed genes using microarray technology. The  
CC present sequence represents a cDNA encoding a human PRO protein of the  
XX invention  
XX  
SQ Sequence 932 BP; 239 A; 241 C; 214 G; 237 T; 0 U; 1 Other;  
Query Match 72.2%; Score 353; DB 6; Length 932;  
Best Local Similarity 84.0%; Pred. No. 3.4e-103;  
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;  
QY 4 TGAGGCTAGATCTTCAGAACTGTCCTTCTGGAGGACCTGGTCCAACTTTCATCAGGCCT 62  
Db 229 TGGGGCTGAGTCTCCAGAACTGTCCTTCTGGAGGACCTGGTCCAACTTTCATCAGGCAC 288

QY 63 ATACTGCTATTATCATAGACTTCAGCAAACTCTCTCAAGGATGATTTGGCCAAACACTT 122  
DB 289 ATACCACTGTCATATAGACTTCGACCAAACTCTCAAGGATGATTTGGCCAAACACTT 348  
QY 123 TCGGTGGTTTACTCAGCTCAGACTCTGATACCAAGATGTTCCCTGCTGGAG 182  
DB 349 TCGGTGGTTTACTCAGCTCAGACTCTGATACCAAGATGTTCCCTGCTGGAG 408  
QY 183 GTAGTATGCTGGCAAGTTACTTCTTTCAGGACAGCAGATTTCGCCAGGGCCAA 242  
DB 409 GAATTAATGCTGATATCTATCACTCTTATATAGACACCAAACTCTGCAAGGGCCAA 468  
QY 243 GGGACCTTTGCAATAGCACTGGAAGCCAGCAAAATGTTCTGTGAGACGGATCTTGTCAT 302  
DB 469 AGAACCTTTGCAATAGCACTGGAAGCCAGCAAAATGTTCTGTGAGATGATCTTGTCAT 528  
QY 303 CTGACGGTCTGCTTTTTCAGTGGCTTTCTGCTGATGCTTCCATGGATCAAGTGA 362  
DB 529 CTGATGCTCAGGCTTTTTCAGTGGCTTTCTGCTGATGCTTCCATGGATCAAGTGA 588  
QY 363 TGAGGACGGCTCATTTTCACTGCTTATGCTTCTTTGGGATCTGGGATCCACCACGCTAG 422  
DB 589 TGCGCAGGCTGCTTCTCACTGCTTATGCTTCTTTGGGATCTGGGATCCACCACGCTAT 648  
QY 423 CCATCTNCATCTACTTTGGGGAACCCAGCGCGGAAAGCCAGGCTTATGAGCCACAC 482  
DB 649 CCGTCTCCATCTGCTTTGGGCGACCCAGCGCGGAAAGCCAGGCTTATGAGCACTACAT 708  
QY 483 AAGACTT 489  
DB 709 AGTCTT 715  
RESULT 12  
ACAS7990  
ID ACA57990 standard; cdna; 932 BP.  
AC ACA57990;  
XX  
XX 09-JUN-2003 (first entry)  
XX  
XX cdna encoding human neoplasia inhibiting PRO polypeptide PRO240.  
XX Human; s; gene; tumour; cancer; neoplasia; liver cancer; sarcoma;  
XX breast cancer; ovarian cancer; renal cancer; colorectal cancer; melanoma;  
XX uterine cancer; prostate cancer; lung cancer; bladder cancer; leukaemia;  
XX gastric cancer; pancreatic cancer; vulval cancer; thyroid cancer;  
XX central nervous system cancer; hepatic carcinoma; glioblastoma;  
XX neuronal disorder; glial disorder; astrocytal disorder;  
XX hypothalamic disorder; glandular disorder; macrophagal disorder;  
XX epithelial disorder; stromal disorder; blastocoelic disorder;  
XX inflammatory disorder; angiogenic disorder; immunologic disorder.  
XX  
XX Homo sapiens.  
XX  
XX US2002192209-A1.  
XX  
XX 19-DEC-2002.  
XX  
XX 30-NOV-2001; 2001US-00001054.  
XX  
XX 17-SEP-1997; 97US-0059114P.  
XX 27-MAR-1998; 98US-0079689P.  
XX 30-MAR-1998; 98US-007920P.  
XX 24-APR-1998; 98US-008299P.  
XX 29-APR-1998; 98US-0083545P.  
XX 12-MAY-1998; 98US-0085149P.  
XX 02-JUN-1998; 98US-0087607P.  
XX 11-JUN-1998; 98US-0088858P.  
XX 25-JUN-1998; 98US-0090691P.  
XX 17-AUG-1998; 98US-0096891P.  
XX 17-AUG-1998; 98US-0096894P.  
PR 10-SEP-1998; 98US-0099803P.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98US-0100263P.  
PR 15-SEP-1998; 98US-0100380P.  
PR 23-SEP-1998; 98US-0101476P.  
PR 10-NOV-1998; 98US-0107783P.  
PR 18-NOV-1998; 98US-0108849P.  
PR 19-NOV-1998; 98US-00180097.  
PR 15-DEC-1998; 98US-0112420P.  
PR 22-DEC-1998; 98US-00218517.  
PR 22-DEC-1998; 98US-0113296P.  
PR 05-JAN-1999; 98WO-US000106.  
PR 12-JAN-1999; 99US-0115554P.  
PR 12-JAN-1999; 99US-0115558P.  
PR 20-JAN-1999; 99US-0116533P.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99US-0123618P.  
PR 12-APR-1999; 98US-00284291.  
PR 20-APR-1999; 98WO-US008615.  
PR 27-APR-1999; 99US-0131294P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 22-JUN-1999; 99US-0140650P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 25-AUG-1999; 99US-00380137.  
PR 25-AUG-1999; 99US-00380138.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 09-SEP-1999; 99US-00380913.  
PR 18-OCT-1999; 99US-00403297.  
PR 29-OCT-1999; 99US-0152506P.  
PR 10-NOV-1999; 99US-00423741.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 09-DEC-1999; 99US-0170262P.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030099.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 03-MAR-2000; 2000US-0187202P.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 08-NOV-2000; 2000US-00709238.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872034.  
PR 01-JUN-2001; 2001US-00872035.  
PR 14-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001US-00882636.  
PR 29-JUN-2001; 2001WO-US019692.  
PR 09-JUL-2001; 2001WO-US021066.  
PR 30-JUL-2001; 2001US-00518585.  
PR 06-AUG-2001; 2001US-00524419.  
PR 09-AUG-2001; 2001US-00527796.  
PR 13-AUG-2001; 2001US-00529404.  
PR 28-AUG-2001; 2001US-00941992.  
PR 29-AUG-2001; 2001WO-US027099.

```
PR 04-SEP-2001; 2001US-00946374.
PA (GETH ) GENENTECH INC.
PI Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
PI Shelton DL, Smith V, Watanabe CK, Wood WI;
XX WPI; 2003-328851/06.
DR P-PSDB; ABU71416.
XX
XX Novel isolated PRO polypeptides e.g. PRO240, PRO381, PRO540, useful for
PT treating tumor, preferably cancer, or for treating neuronal, glial,
PT hypothalamic, stromal, inflammatory, angiogenic and immunologic
PT disorders.
XX
XX Claim 20; Fig 1; 186pp; English.
XX
XX The invention relates to an isolated secreted and transmembrane
CC polypeptide, designated as PRO polypeptide, PRO polypeptide lacking its
CC associated signal peptide or PRO polypeptide extracellular domain with or
CC without its associated signal peptide. The PRO polypeptide or an antibody
CC binding to it is useful for inhibiting the growth of a tumor cell. A
CC composition containing a PRO polypeptide is useful for inhibiting
CC neoplastic cell growth or for treating a tumor, preferably cancer (such
CC as liver, breast, ovarian, renal, colorectal, uterine, prostate, lung,
CC bladder, gastric, pancreatic, vulval, colorectal, thyroid, central nervous system
CC cancer, hepatic carcinomas, sarcomas, glioblastomas, melanoma or
CC leukaemia) in a mammal. The PRO polypeptide is useful for identifying its
CC agonists. The PRO polypeptide or an antibody binding to it is useful in
CC the preparation of a medicament for treating a condition which is
CC responsive to the PRO polypeptide or an antibody binding to it. The PRO
CC polypeptide or an antibody binding to it is also useful for treating
CC neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal,
CC epithelial, stromal, blastocytic, inflammatory, angiogenic and
CC immunologic disorders. The present sequence represents a cDNA encoding a
CC PRO polypeptides of the invention
XX
XX Sequence 932 BP; 239 A; 241 C; 214 G; 237 T; 0 U; 1 Other;
XX
Query Match 72.2%; Score 353; DB 7; Length 932;
Best Local Similarity 84.0%; Pred. No. 3.4e-103;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;
XX 4 TGAGGCTAGACTCTTCAGAACTGTTCCTT-GAGGATCCTGGTCCAAACTTTTACAGGCTT 62
DB 229 TGGGGTGTGATCTCCAGACTGTCTCTCGAGGACCTGTCCAACTTTCATCAGGCAC 288
XX 63 ATACTGCTATTATCATAGACCTTCAGGAAATCCTCTCAAGGATGATTTGGCCAAACCT 122
DB 289 ATACCACCTGTATCATAGACCTTCAGGAAACCCCTCAAGGTGACTTTGGCCAAACCT 348
XX 123 TCGTGGGTTTACTCAGCTGCAGACTCTGATACCTACCAAGATGTCCTGTCTGTGGAG 182
DB 349 TCGTGGCTTTTACTCAGCTCCAGACTCTGATCTGCGACCAACATGTCAACTGTCTGTGG 408
XX 183 GTAGTAATGCTGGGCAATGTACTTCTTTCAAGGACCAAGCAGATTTGCCAAGGGCAAA 242
DB 409 GAATTAATGCTGGAATCATCATCCTCTTATATAGAACCAAAATCTGTCAAGGGCAAA 468
XX 243 GGCACCTTTCATAGACTGAGAGCCGAGAAATGTCTGTGACGATCTTGTGCTAT 302
DB 469 AGAACCTTTGCAATAACACTTGGGGACCCGAAATGTCTGTGAGATGATCTTGTGTAC 528
XX 303 CTACACGCTCTGCTCTTTTGCAGTGGGTTTGTCTGATGTTTCCATGATCAACAGTGTA 362
DB 529 CTGATGCTCAGGCTCTTTTGCAGTGTGTTTGTCTGATGTTTCCATGATCAACAGTGTA 588
XX 363 TGAGGACGGGCTCATTTTCTGCTTATGTTCTTTTGGGATCTGGGATCCACACGCTAG 422
DB 589 TGGGCCAGGGCTGGTCTCACTGCTTATGTTCTTGGGATTTCTGGGAGCCACCACTCTAT 648
XX 423 CCATCTNCATCTTACTTTGGGAAACCCAGCGCGGAAAGCCAAAGGCTTATGAGCCACAC 482
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Db 649 CCGTCTCCATTCTGTTTGGGCGACCGCGCGAAGCCAAAGACTTCTATGAATACAT 708
Qy 483 AAGACTT 489
Db 709 AGGTCTT 715
RESULT 13
IDA01275
XX ADA01275 standard; cDNA; 932 BP.
AC ADA01275;
XX 06-NOV-2003 (first entry)
XX Human PRO polynucleotide #4.
XX
XX Human; Gene; ss; secreted polypeptide; transmembrane polypeptide;
XX tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
XX adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
XX microvascular endothelial cell; endothelial cell tube formation;
XX sports-related joint problem; articular cartilage defect; osteoarthritis;
XX rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
XX
XX Homo sapiens.
XX
XX US2003068779-A1.
XX 10-APR-2003.
XX 16-SEP-2002; 2002US-00245107.
XX 09-MAY-2001; 2001US-0290589P.
XX 29-AUG-2001; 2001WO-US027099.
XX 18-JUL-2002; 2002US-00197942.
XX (GETH ) GENENTECH INC.
XX Baker KP, Eaton DL, Filvaroff B, Goddard A, Grimaldi JC;
XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
XX Fong S;
XX WPI; 2003-625484/59.
XX P-PSDB; ADA01276.
XX Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
XX stimulating proliferation of human microvascular endothelial cells, and
XX PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
XX cells.
XX Claim 2; Fig 7; 307pp; English.
XX
XX The invention relates to isolated human PRO polypeptides (secreted and
XX transmembrane polypeptides) and the polynucleotides encoding them. The
XX invention also relates to an antibody which specifically binds to a PRO
XX polypeptide, a method for stimulating the release of tumour necrosis
XX factor-alpha (TNF-alpha) from human blood, a method for stimulating the
XX proliferation or differentiation of chondrocyte cells and a method for
XX detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
XX colon, breast, prostate, rectal, cervical and liver tumours). The
XX polynucleotides are useful in molecular biology, including uses as
XX hybridisation probes, in chromosome and gene mapping, in generating
XX antisense RNA and DNA and in gene therapy. The polynucleotides may also
XX be used in preparing PRO polypeptides by recombinant techniques and in
XX generating either transgenic animals or knock-out animals which are
XX useful in the development and screening of therapeutically useful
XX reagents. The PRO polypeptides or antibodies are used in preparing a
XX medicament for treating a condition responsive to the polypeptides or
XX antibodies, such as tumours, for stimulating and inhibiting proliferation
XX of human microvascular endothelial cells, for inducing endothelial cell
XX tube formation and for treating sports-related joint problems, articular
XX cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
XX represents a human PRO polynucleotide of the invention.
```

XX	Sequence	932 BP; 239 A; 241 C; 214 G; 237 T; 0 U; 1 Other;	
XX	Query Match	72.2%; Score 353; DB 8; Length 932;	
XX	Best Local Similarity	84.0%; Pred. No. 3.4e-103;	
XX	Matches	409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;	
QY	4	TAAGCTAGATCTTCAGAACTGTTCCCT-GAGGATCTGTGTCACAACTTTTACAGGCTT 62	
DB	229	TGGGGCTGGATCTCCAGAACTGTTCTCTGGAGGACCTGTGTCACAACTTTTCATCAGGCAC 288	
QY	63	ATACCTGCTATTATCATACACCTTCAGGCAAACTCTCTCAAGGATGATTGGCCCAACCT 122	
DB	289	ATACACCTGTCATCATAGACCTGCAAGCAACCCCTCAAGGTGACTTGGCCCAACCT 348	
QY	123	TCCGTGGGTTTACTCAGCTGCAGACTCTGTATACCAAGATGTTCCCTGTCTCTGGAG 182	
DB	349	TCCGTGGGTTTACTCAGCTGCAGACTCTGTATACCAAGATGTTCCCTGTCTCTGGAG 408	
QY	183	GTAGTAATGCTGGGACAACTGTTACTTCTTTCAGGGACAGACATTTGCCAGGGCAA 242	
DB	409	GAATTAATGCTGGGACAACTGTTACTTCTTTCAGGGACAGACATTTGCCAGGGCAA 468	
QY	243	GGGACCTTTTGAATAGCACTGGAAAGCCAGAAATGTCTCTGAGAACGGATCTTGTGCAT 302	
DB	469	AGAACCTTTTGAATAGCACTGGGACCCAGAAATGTCTCTGAGAACGGATCTTGTGTAC 528	
QY	303	CTGACGGTCCGCTTTTTCAGTGGCTTTGTGTGATGTTTCCATGGATACAAGTGA 362	
DB	529	CTGATGGTCCAGGCTTTTTCAGTGGCTTTGTGTGATGTTTCCATGGATACAAGTGA 588	
QY	363	TGAGGCGAGGCTCATTTTCACTGTTTATGTTTCTTTGGGATTCGGGATCCACCACGCTAG 422	
DB	589	TGCGCCAGGCTCGTTTCTCACTGTTTATGTTTCTTTGGGATTCGGGATCCACCACCTAT 648	
QY	423	CCATCTTCATCTCACTTTTGGGACCCAGCGCCGGAAGCCAAAGCTTNNATGAGCCACAC 482	
DB	649	CCGCTTCATCTCTGTTTGGGACCCAGCGCCGGAAGCCAAAGCTTNNATGAGCTAT 708	
QY	483	AAGACTT 489	
DB	709	AGGCTT 715	
RESULT 14	ADA43704	standard; cDNA; 932 BP.	
XX	ADA43704;		
XX	AC		
XX	AD		
XX	20-NOV-2003	(first entry)	
XX	Human cDNA encoding secreted/transmembrane polypeptide PRO240.		
DE	ss; gene; human; PRO; secreted protein; transmembrane polypeptide PRO240.		
XX	endothelial cell tube formation; chondrocyte cell differentiation;		
KW	microvascular endothelial cell; tumour; lung tumour; colon tumour;		
KW	breast tumour; prostate tumour; rectal tumour; kidney tumour;		
KW	liver tumour; cytostatic; vaccine.		
XX	Homo sapiens.		
OS	US2003064474-A1.		
XX	03-APR-2003.		
XX	16-SEP-2002; 2002US-00245859.		
XX	29-AUG-2001; 2001WO-US027099.		
PR	18-JUL-2002; 2002US-00197942.		
XX	(GETH ) GENENTECH INC.		

Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC, Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z, Fong S; WPI; 2003-605867/57. P-PSDB; ADA43705.

New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or PRO1383, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.

Claim 2; Fig 7; 308pp; English.

The invention relates to an isolated secreted/transmembrane (PRO) polypeptide, having at least 80% sequence identity to a sequence selected from any one of the 57 amino acid sequences given in specification, or to a sequence encoded by a nucleic acid molecule selected from any one of the nucleic acids deposited under any of the ATCC accession numbers given in specification, or a sequence having at least 80% identity to PRO lacking its associated signal peptide, an extracellular domain of PRO with or without its associated signal peptide. Also included are vectors, transformed host cells, anti-PRO antibodies, the nucleic acids encoding PRO, PRO fusion proteins, inducing endothelial cell tube formation (by administering PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6000, and PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and an oligonucleotide probe derived from any one of the above nucleotide sequences. PRO6018 polypeptide is useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080 and PRO21383 polypeptides are useful for stimulating the proliferation of human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006 polypeptides are useful for inhibiting the proliferation of human microvascular endothelial cells. PRO polypeptides are useful for detecting the presence of tumour in a mammal, including tumours of lung, colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and PRO34274 polypeptides are useful for inducing endothelial cell tube formation. PRO or the antibody are useful in the preparation of a medicament for treating a condition responsive to PRO polypeptide. The oligonucleotide probes are useful for isolating genomic and cDNA nucleotide sequences, for measuring or detecting the expression of an associated gene, and as antisense probes. PRO nucleic acid is useful as a hybridisation probe, in chromosome and gene mapping, in the generation of antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The present sequence encodes a PRO protein.

XX SQ Sequence 932 BP; 239 A; 241 C; 214 G; 237 T; 0 U; 1 Other;

Query Match 72.2%; Score 353; DB 8; Length 932; Best Local Similarity 84.0%; Pred. No. 3.4e-103; Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

QY 4 TGAGCTAGATCTTCAGAACTGTTCCCT-GAGGATCTGTGTCACAACTTTTACAGGCTT 62

DB 229 TGGGGCTGGATCTCCAGAACTGTTCTCTGGAGGACCTGTGTCACAACTTTTCATCAGGCAC 288

QY 63 ATACTGCTATTATCATACACCTTCAGGCAAACTCTCTCAAGGATGATTGGCCCAACCT 122

DB 289 ATACACCTGTCATCATAGACCTGCAAGCAACCCCTCAAGGTGACTTGGCCCAACCT 348

QY 123 TCCGTGGGTTTACTCAGCTGCAGACTCTGTATACCAAGATGTTCCCTGTCTCTGGAG 182

DB 349 TCCGTGGGTTTACTCAGCTGCAGACTCTGTATACCAAGATGTTCCCTGTCTCTGGAG 408

QY 183 GTAGTAATGCTGGGACAACTGTTACTTCTTTCAGGGACAGACATTTGCCAGGGCAA 242

DB 409 GAATTAATGCTGGGACAACTGTTACTTCTTTCAGGGACAGACATTTGCCAGGGCAA 468

QY 243 GGGACCTTTGCAATAGCACTGGAAAGCCAGAAATGTCTCTGAGAACGGATCTTGTGCAT 302

DB 469 AGAACCTTTGCAATAGCACTGGGACCCAGAAATGTCTCTGAGAACGGATCTTGTGTAC 528

QY 303 CTGACGGTCCGCTTTTTCAGTGGCTTTGTGTGATGTTTCCATGGATACAAGTGA 362

DB 529 CTGATGGTCCAGGCTTTTTCAGTGGCTTTGTGTGATGTTTCCATGGATACAAGTGA 588

QY 363 TGAGGCGAGGCTCATTTTCACTGTTTATGTTTCTTTGGGATTCGGGATCCACCACGCTAG 422

DB 589 TGCGCCAGGCTCGTTTCTCACTGTTTATGTTTCTTTGGGATTCGGGATCCACCACCTAT 648

QY 423 CCATCTTCATCTCACTTTTGGGACCCAGCGCCGGAAGCCAAAGCTTNNATGAGCCACAC 482

DB 649 CCGCTTCATCTCTGTTTGGGACCCAGCGCCGGAAGCCAAAGCTTNNATGAGCTAT 708

QY 483 AAGACTT 489

DB 709 AGGCTT 715

RESULT 14

ADA43704

ADA43704 standard; cDNA; 932 BP.

XX ADA43704;

XX AC

XX AD

XX 20-NOV-2003 (first entry)

XX Human cDNA encoding secreted/transmembrane polypeptide PRO240.

DE ss; gene; human; PRO; secreted protein; transmembrane polypeptide PRO240.

XX endothelial cell tube formation; chondrocyte cell differentiation;

KW microvascular endothelial cell; tumour; lung tumour; colon tumour;

KW breast tumour; prostate tumour; rectal tumour; kidney tumour;

KW liver tumour; cytostatic; vaccine.

XX Homo sapiens.

OS US2003064474-A1.

XX 03-APR-2003.

XX 16-SEP-2002; 2002US-00245859.

XX 29-AUG-2001; 2001WO-US027099.

PR 18-JUL-2002; 2002US-00197942.

XX (GETH ) GENENTECH INC.

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Dd 529 CTGATGGTCCAGGCTCTTTGCAAGTGTGTTGGCTGATGGTTTCATGGATACAGTGTA 588
Qy 363 TGAGGCAGGGCTCATTCTTCACTGCTTATGCTTTCTTTGGGATTCGGATCCACCAAGCTAG 422
Dd 589 TGGCCAGGGCTCGTCTCAGTCTTATGTTTCTTGGGATTCGGGATTCGGAGCCCACTCTAT 648
Qy 423 CCATCTNCAATTTACTTTGGGGAACCCAGCGCGGAAAGCCAAAGCTTATGAGCCACAC 482
Dd 649 CCGTCTCCATTTCTGCTTTGGGCGACCCAGCGCGGAAAGCCAAAGCTTATGAGCTATACAT 708
Qy 483 AAGACTT 489
Dd 709 AGGTCTT 715

RESULT 15
ADA43472
ID ADA43472 standard; cDNA; 932 BP.
XX AC ADA43472;
XX DT 20-NOV-2003 (first entry)
XX DE Human cDNA encoding secreted/transmembrane polypeptide PRO240.
XX ss; gene; human; PRO; secreted protein; transmembrane protein;
XX endotheial cell tube formation; chondrocyte cell differentiation;
XX microvascular endothelial cell; tumour; lung tumour; colon tumour;
XX breast tumour; prostate tumour; rectal tumour; kidney tumour;
XX liver tumour; cytostatic; vaccine.
XX OS Homo sapiens.
XX PN US2003073196-A1.
XX PD 17-APR-2003.
XX PF 18-SEP-2002; 2002US-00246210.
XX PR 04-APR-2001; 2001US-0282199P.
XX PR 29-AUG-2001; 2001WO-US027099.
XX PR 18-JUL-2002; 2002US-00197942.
XX PA (GETH ) GENENTECH INC.
XX PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX DR WPI; 2003-743814/70.
XX DR P-PSDB; ADA43473.
XX PT New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
XX PT PRO21383 useful for stimulating the proliferation or differentiation of
XX PT chondrocyte cells and detecting the presence of a tumor in a mammal.
XX PS Claim 2; Fig 7; 307pp; English.
XX CC The invention relates to an isolated secreted/transmembrane (PRO)
XX CC polypeptide, having at least 80% sequence identity to a sequence selected
XX CC from any one of the 57 amino acid sequences given in specification, or to
XX CC a sequence encoded by a nucleic acid molecule selected from any one of
XX CC the nucleic acids deposited under any of the ATCC accession numbers given
XX CC in specification, or a sequence having at least 80% identity to PRO
XX CC lacking its associated signal peptide, an extracellular domain of PRO
XX CC with or without its associated signal peptide. Also included are vectors,
XX CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
XX CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
XX CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
XX CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
XX CC an oligonucleotide probe derived from any one of the above nucleotide
XX CC sequences. PRO6018 polypeptide is useful for stimulating the
```

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CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumour in a mammal, including tumours of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO381, PRO1560,
CC PRO189, PRO4499, PRO6308, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
XX present sequence encodes a PRO protein.
XX Sequence 932 BP; 239 A; 241 C; 214 G; 237 T; 0 U; 1 Other;
SQ
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Query Match 72.2%; Score 353; DB 8; Length 932;  
Best Local Similarity 84.0%; Pred. No. 3.4e-103;  
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

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Qy 4 TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCCTGGTCCAAACTTTTACAGGCTT 62
Dd 229 TGGGGCTGGATCTCCAGAACTGTTCTCTGGAGACCTGTCTCCAACTTTCATCAGGCAC 288
Qy 63 ATACTGCTATPATCATAGACTTCAGGCAAAATCTCTCAAGGATGATTTGGCCAAACCT 122
Dd 289 ATACCAGTGTCTCATAGACTGCTGCAAGCAAAACCCCTCAAAGGTGACTTGGCCAAACCT 348
Qy 123 TCCGTGGGTTTACTCAGCTGCAGACTCTGATACCAAGAGATGTTCCCTGCTCTGGAG 182
Dd 349 TCCGTGGCTTTACTCAGCTGCAGACTCTGATACCTGCTGATGCTGCTGCTGCTGAG 408
Qy 183 GTAGTAATGCTCGGACAAATGTTACTTCTTCAAGGACAAAGCAGATTGGCAAGGCAAA 242
Dd 409 GAATTATGCTCGGATGATATCACTCTTATATAGACACCAAAATCTGTCAAGGGCAAA 468
Qy 243 GGGACCTTTGCAATAGCACTGGAGCCGAGAAATGTCTCTGAGAACGGATCTTGTGCAT 302
Dd 469 AGAACCTTTGCAATAACACTGGGACCCGAGAAATGTCTCTGAGATGGATCTTGTGTAC 528
Qy 303 CTGACGGTCTGGTCTTTTGGCAGTGGCTTGTGCTGATGGTTCCTATGGATACAAAGTGA 362
Dd 529 CTGATGCTCAGGCTCTTTTGGCAGTGGTGTGCTGATGGTTCCTATGGATACAAAGTGA 588
Qy 363 TGAGGCAGGGCTCAATTTCACTGCTTATGTTCTTTGGGATTTCTGGATTCACCAAGCTAG 422
Dd 589 TGGCCAGGGCTCGTCTCTCACTGCTTATGTTCTTGGGATTTCTGGAGCCCACTCTAT 648
Qy 423 CCATCTNCAATTTACTTTGGGGAACCCAGCGCGGAAAGCCAAAGCTTATGAGCCACAC 482
Dd 649 CCGTCTCCATTTCTGCTTTGGGCGACCCAGCGCGGAAAGCCAAAGCTTATGAGCTATACAT 708
Qy 483 AAGACTT 489
Dd 709 AGGTCTT 715
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Search completed: June 25, 2004, 22:17:58  
Job time : 727 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 21:55:07 ; Search time 1995 Seconds

(without alignments)  
7319.602 Million cell updates/sec

Title: US-09-773-476-294

Perfect score: 489

Sequence: 1 gactgaggtagatcttcag.....tnatgagccacacaagactt 489

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_hco:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_man:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_pbg:\*

27: em\_gss\_vil:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

# SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	487	99.6	489	29	CG539763 OST131079
2	476	97.3	486	29	CG615808 OST1307322
3	472	96.5	763	13	BUS57697 AGENCOURT
4	471.4	96.4	512	9	AA017836 mh44h03.r

5	471.4	96.4	762	14	CD364102
6	471.4	96.4	791	9	AU080019
7	471.4	96.4	838	14	CK128347
8	471.4	96.4	884	11	BC038336
9	469.8	96.1	933	11	AK002276
10	459.4	93.9	614	9	AA108529
11	458.6	93.8	754	12	BG142354
12	456.2	93.3	669	10	BE994240
13	449.2	91.9	635	29	CG589400
14	447.8	91.6	720	13	BQ748981
15	446.4	91.3	469	13	BX520494
16	445.4	91.1	671	9	AI116932
17	432.2	88.4	616	10	BE985460
18	432.6	86.6	640	14	CA452314
19	415.8	85.0	614	10	BF462535
20	412.2	84.3	475	9	AI115639
21	410.8	84.0	470	9	AA796965
22	397	81.2	724	13	BQ199079
23	395.4	80.9	425	9	AA450686
24	394.4	80.7	483	9	AA273740
25	394.4	80.7	1039	14	W15719
26	393	80.4	499	10	BE848379
27	382.4	78.2	566	10	AW908899
28	381.6	78.0	605	10	BE956564
29	378.4	77.4	637	13	BY744162
30	369.4	75.5	460	10	BE852127
31	369.4	75.5	592	9	AW044815
32	362	74.0	407	10	BE861531
33	359.2	73.5	983	10	BF568872
34	358	73.2	902	14	CF587266
35	354.6	72.5	551	13	BQ305549
36	353.8	72.4	1048	9	AL560711
37	353.6	72.3	836	13	BQ716341
38	353	72.2	561	13	BQ305554
39	353	72.2	566	13	BQ305557
40	353	72.2	582	13	BQ305556
41	353	72.2	590	13	BQ305551
42	353	72.2	591	10	AW912084
43	353	72.2	748	13	BUS40754
44	353	72.2	752	14	CB957744
45	353	72.2	758	12	BI760599

## ALIGNMENTS

RESULT 1  
CG539763  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

CG539763 489 bp DNA linear GSS 01-OCT-2003

OST131079 Mus musculus 129Sv/Ev Mus musculus genomic clone

OST131079, genomic survey sequence.

CG539763 GI:37326335

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 489)

Zambrowicz, B., Abuin, A., Ramirez-Solis, R., Richter, L.J.,

Piggott, C.J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,

Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,

Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,

Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,

Sparks, M.J., van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,

Zhu, Q., Person, C. and Sands, A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap

screen to identify potential targets for therapeutic intervention

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

Contact: Zambrowicz BP

OmiBank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com  
Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
described in Zambrowicz et al (Nature. 1998 Apr 9;352(6576):608-11)  
Class: Gene Trap.

[illegible]

## ORIGIN

Query Match	99.6%	Score 487	DB 29	Length 489
Best Local Similarity	100.0%	Pred. No. 6.5e-136		
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QY	1	GACTCAGCTAGATCTTCAGAACCTTCCAGGAAATCCCTCTCAAGGATGATTTGGCCCAAC	60	
DB	1	GACTCAGCTAGATCTTCAGAACCTTCCCTGAGGATCCTGGTCCAAACTTTTACAGGC	60	
QY	61	TTATACTCTATTTATCATAGACCTTCAGGCAATCCCTCTCAAGGATGATTTGGCCCAAC	120	
DB	61	TTATACTCTATTTATCATAGACCTTCAGGCAATCCCTCTCAAGGATGATTTGGCCCAAC	120	
QY	121	CTTCGCTGGTTTACTCAGCTCGACACTCTGATACTACACAGATGTTCCCTGCTCTGG	180	
DB	121	CTTCGCTGGTTTACTCAGCTCGACACTCTGATACTACACAGATGTTCCCTGCTCTGG	180	
QY	181	AGGTAGTAATGCCTGGGCAATGTTACTCTCTTCAAGGCAAGCAGATTTGCCAAGGCA	240	
DB	181	AGGTAGTAATGCCTGGGCAATGTTACTCTCTTCAAGGCAAGCAGATTTGCCAAGGCA	240	
QY	241	AAGGACACCTTTGCAATAGCACTGGAAGCCAGAAATGTTCTCTGAGAACGGATCTTGTC	300	
DB	241	AAGGACACCTTTGCAATAGCACTGGAAGCCAGAAATGTTCTCTGAGAACGGATCTTGTC	300	
QY	301	ATCTCAGCGTCTCGTCTTTTCAGTCGCTTGTCTGATGTTTCCATPGNATCAAGTG	360	
DB	301	ATCTCAGCGTCTCGTCTTTTCAGTCGCTTGTCTGATGTTTCCATPGNATCAAGTG	360	
QY	361	TATGAGGCAGGGCTCATTTTCACCTGCTATGTTCTTTGGGATCTTGGGATCCACACGCT	420	
DB	361	TATGAGGCAGGGCTCATTTTCACCTGCTATGTTCTTTTGGGATCTTGGGATCCACACGCT	420	
QY	421	AGCCATCTNCAATTTACTTTGGGAAACCCAGCGCCGGAAGCCAAAGGCTTTNATGAGCCAC	480	
DB	421	AGCCATCTNCAATTTACTTTGGGAAACCCAGCGCCGGAAGCCAAAGGCTTTNATGAGCCAC	480	
QY	481	ACAAAGCTTT 489		
DB	481	ACAAAGCTTT 489		

CG615908	CG615908	496 bp	DNA	linear	GSS 02-OCT-2003
LOCUS	OSR307322	Mus musculus I29SV/EV	Mus	musculus genomic clone	
DEFINITION	OSR307322	genomic survey sequence.			
ACCESSION	CG615908				
VERSION	CG615908.1	GI:37439757			
KEYWORDS	GSS.				

ORGANISM	<i>Mus musculus</i>
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 496)
AUTHORS	Zambrozic, B.P., Abuln, A., Ramirez-Solis, R., Richter, L.J., Piggett, J., Baltangelio, H., Buxton, E.C., Edwards, J., Finch, R.A., Fridle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W., Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,

TITLE	JOURNAL	COMMENT
1. The Role of the Teacher in the Classroom	Journal of Educational Research	1965, Vol. 68, No. 1, pp. 1-10
2. The Impact of Technology on Education	Journal of Educational Technology	1978, Vol. 1, No. 2, pp. 1-10
3. The Importance of Parental Involvement	Journal of Educational Psychology	1985, Vol. 77, No. 3, pp. 1-10
4. The Effect of Teacher Expectations on Student Achievement	Journal of Educational Research	1990, Vol. 93, No. 1, pp. 1-10
5. The Role of the School in the Community	Journal of Educational Research	1995, Vol. 98, No. 1, pp. 1-10
6. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	2000, Vol. 103, No. 1, pp. 1-10
7. The Role of the Teacher in the 21st Century	Journal of Educational Research	2005, Vol. 108, No. 1, pp. 1-10
8. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	2010, Vol. 113, No. 1, pp. 1-10
9. The Role of the Teacher in the 21st Century	Journal of Educational Research	2015, Vol. 118, No. 1, pp. 1-10
10. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	2020, Vol. 123, No. 1, pp. 1-10

## FEATURES

## ORIGIN

Query Match	97.3%	Score 476;	DB 29;	Length 496;
Best Local Similarity	99.6%;	Prod. No. 1.4e-132;		
Matches 476;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	12	GATCTTCAGAACTGTTCCCTCGAGAGTCCCTGGTCCAAACCTTTTACAGGCTTATACGTGCTA	71	
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QY	72	TTATCATAGACCTTTCAGGCAAAATCTCTCTCAAGGATGATTTGGCCAAACCTTTCGCTGGGT	131	
Db	68	TTATCATAGACCTTTCAGGCAAAATCTCTCTCAAGGATGATTTGGCCAAACCTTTCGCTGGGT	127	
QY	132	TTACTCAGCTCGACAGCTCATACTACTACCAAGATGCTCCCTGTCTCTCGAGGTAGTAAATG	191	
Db	128	TTACTCAGCTCGACAGCTCATACTACTACCAAGATGCTCCCTGTCTCTCGAGGTAGTAAATG	187	
QY	192	CTCGGACAATGTACTCTCTTCAAGACAAGCAGATTTGCCAAGGCAAGGGACCTTT	251	
Db	188	CTCGGACAATGTACTCTCTTCAAGACAAGCAGATTTGCCAAGGCAAGGGACCTTT	247	
QY	252	GCAATAGACATCGGAAGCCCAAGAAATGTCTCTGAGAACGGATCTTGTGCATCTGACGCTC	311	
Db	248	GCAATAGACATCGGAAGCCCAAGAAATGTCTCTGAGAACGGATCTTGTGCATCTGACGCTC	307	
QY	312	CTGTGCTTTTTCAGTGGGTTTGTGCTGATGGTTTCCATGGATCAAGTGTATGAGGCAGG	371	
Db	308	CTGTGCTTTTTCAGTGGGTTTGTGCTGATGGTTTCCATGGATCAAGTGTATGAGGCAGG	367	
QY	372	GCTCATTTTTCAGTGCCTTATGTTCTTTTGGGATCTCTGGATCCACCGCTAGGCCATCTNCA	431	
Db	368	GCTCATTTTTCAGTGCCTTATGTTCTTTTGGGATCTCTGGATCCACCGCTAGGCCATCTCCA	427	
QY	432	TTTCTACTTTTGGGGAACCCAGCGCGGAAAGCCAAAGCTTTNATGAGCCACACAAGACTT	489	
Db	428	TTTCTACTTTTGGGGAACCCAGCGCGGAAAGCCAAAGCTTTNATGAGCCACACAAGACTT	485	

RESULT 3	ACCESSION
BU557697	VERSION
LOCUS	KEYWORDS
DEFINITION	SOURCE
	ORGANISM

BU557697 763 bp mRNA linear EST 16-SEP-2002  
 AGENCOURT 10187185 NIH\_MGC\_144 Mus musculus cDNA clone  
 IMAGE:6585654 5', mRNA sequence.



Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 763)  
NIH-MGC <http://mgi.nci.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein  
cDNA Library Preparation: Michael Brownstein Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM2797 row: p column: 06  
High quality sequence stop: 579.  
Location/Qualifiers  
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by oligo-dT priming and directionally cloned. 5' and 3'  
adaptors were used in cloning as follows:  
5'-AAGCAGTGTATCAACGAGTGGCCATTCAGCGCGG-3' and  
5'-ATTCAGAGCGCGCGGCGACATG-dt(30)NN-3'. Full-length  
enriched library was constructed using the Clontech  
Creator SMART kit and size-selected to contain the 0.2-0.5  
kb size fraction (other fractions present in NIH\_MGC\_143).  
Library created in the laboratory of M. Brownstein (NIMH,  
NIH). Note: this is a NIH\_MGC Library."

Query Match 96.5%; Score 472; DB 13; Length 763;  
Best Local Similarity 99.4%; Pred. No. 2.8e-131;  
Matches 483; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 5 GAGGCTAGATCTTCAGAACTGTTCCTG-AGGATCTGTGTCACAACTTTTACAGGCTTA 63  
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QY 64 TACTGCTATTATATAGACCTTCAGGCAAACTCTCTCAAGGATGATTTGGCCAAACACCTT 123  
DB 181 TACTGCTATTATATAGACCTTCAGGCAAACTCTCTCAAGGATGATTTGGCCAAACACCTT 240  
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DB 241 CGTGGGTTTACTCAGTCGACACTCTGATACCTACCAAGATGTTCCCTGTCCTGGAGG 300  
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DB 541 CATCTNCACTTACTTTTGGGAAACCCAGCGCGGAAAGCCAAAGGCTTATAGGCCACACACA 600

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

RESULT 4  
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LOCUS  
DEFINITION  
mb44403.r1 Soares mouse placenta 4NBMP13.5 14.5 Mus musculus cDNA  
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ACCSSION  
AA017836  
VERSION  
AA017836.1 GI:1481103  
KEYWORDS  
EST.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 512)  
Marra, M., Hillier, D., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.  
The WashU-HMI Mouse EST Project  
Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mousees@watson.wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
MGI:270733  
Seq primer: -28M13 rev2 from Amersham  
High quality sequence stop: 466.  
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/note="Organ: placenta; Vector: pT73D-Pac (Pharmacia)  
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1st strand cDNA was primed with a Not I - oligo(dT) primer  
[5',  
TGTACCAATCTCAAGTGGAGCGCGGCGGAAATTTTTTTTTTTTTTTTTTTTTT  
T 3']"; double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 96.4%; Score 471.4; DB 9; Length 512;  
Best Local Similarity 99.2%; Pred. No. 3.5e-131;  
Matches 483; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 4 TGAGGCTAGATCTTCAGAACTGTTCCTG-AGGATCTGTGTCACAACTTTTACAGGCTT 62  
DB 506 TGGGGCTAGATCTTCAGAACTGTTCCTGAGGATCTGTGTCACAACTTTTACAGGCTT 447  
QY 63 ATACTGCTATTATCATAGCTTCAGGCAAACTCTCTCAAGGATGATTTGGCCAAACACT 122  
DB 446 ATACTGCTATTATCATAGCTTCAGGCAAACTCTCTCAAGGATGATTTGGCCAAACACT 387

FEATURES  
source

ORIGIN

QY 123 TCCGTGGGTTTACTCAGCTCAGACTCTGATCTACCAAGATGTTCCCTGCTCTGGAG 182  
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 QY 183 GTAGTAAGCTTGGGCAATGTTACTTCTTCAAGGCAAGAGATTTGCCAAGGGCAA 242  
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 QY 363 TGAGGCAAGGCTCAATTTTCACTGCTTATGTTCTTTTGGGATTTCTGGGATCCACACGCTAG 422  
 Db 146 TGAGGCAAGGCTCAATTTTCACTGCTTATGTTCTTTTGGGATTTCTGGGATCCACACGCTAG 87  
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 QY 483 AAGACTT 489  
 Db 26 AAGACTT 20

RESULT 5  
 CD364102  
 LOCUS  
 DEFINITION UI-M-GLO-cfw-n-02-01.r1 NIH BMAP 762 bp mRNA linear EST 15-JUL-2003  
 IMAGE:30358681 5', mRNA sequence.

ACCESSION CD364102  
 VERSION CD364102.1 GI:31144939  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: Dr. Jim Lin, University of Iowa  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Distribution information can be found at  
 http://genome.uiowa.edu/distribution/mousefl.html  
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

The following repetitive elements were found in this cDNA  
 sequence: 258-287, >RUTR5\_MM4LTR/Retroviral (matched complement)  
 Seq primer: PYX-5.  
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 /clone\_lib="NIH\_BMAP\_GLO"  
 /note="Organ: Brain; Vector: pYX-Asc; Site 1: Ecor I; Site 2: Not I; The library was constructed according to Bernaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CCAACTGAAT. This library was created for the University of Iowa Brain Anatomy Project (BMAP). Gene Discovery in the Developing Mouse Nervous System, supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

## ORIGIN

Query Match 96.4%; Score 471.4; DB 14; Length 762;  
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 QY 4 TGAGGCTAGATCTTACAGAACTGTTCCCTG-AGGATCTGTGTCACAACTTTTACAGGCTT 62  
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 QY 243 GGGACCTTTGCAATAGACTGGAAGCCGCAAAATGTCCTGAGAACGAGATCTTGTGCAT 302  
 Db 465 GGGACCTTTGCAATAGACTGGAAGCCGCAAAATGTCCTGAGAACGAGATCTTGTGCAT 524  
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RESULT 6  
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 5', mRNA sequence.  
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 VERSION AU080019.1 GI:6084774  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 791)  
 Hashimoto, K., Kusuda, J., Tanuma, R., Ito, A., Hirata, M., Toyoda, A., Suzuki, Y., Sasaki, M., and Sugano, S.  
 Isolation of full-length cDNA clones from a mouse brain cDNA library made by oligo-capping method  
 Unpublished (1999)  
 JOURNAL  
 COMMENT Contact: Katsuyuki Hashimoto

Division of Genetic Resources  
National Institute of Infectious Diseases  
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan  
Email: [khashinih.go.jp](mailto:khashinih.go.jp)  
URL: <http://www.nih.go.jp/yoken/genbank/>.

## FEATURES source

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cloned into distinct DraIII sites of the pME18S-FL3. XhoI
sites just outside the DraIII sites can be used to isolate
the cDNA insert. Size selection was performed to exclude
fragments <1.5 kb. Library was constructed by Sugano et
al.(University of Tokyo, Institute of Medical Science).
Custom primer used for sequencing: 5' end primer
[CTTCTGCTCTAAAGCTGG], 3' end primer
[CGACCTGCAGCTCGAGACA]"

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Query Match	96.4%;	Score 471.4;	DB 9;	Length 791;
Best Local Similarity	99.4%;	Pred. No. 4.4e-131;		
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QY	4	TGAGCTAGATCTTCAGAACTGTTCCCTG-AGGATCTGTGCCAAACTTTTACAGGCTT	62	
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QY	303	CTGACGGTCCTGGTCTTTTTCAGTCGCTTTGTGTCTGATGTTTCCATGGATACAAGTGT	362	
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Db	622	CCATCTNCATTTCTATTTGGGGAACCCAGCGCCGGAAAGCCAAAGGCTTATGAGCCACAC	681	
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RESULT 7  
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LOCUS	CK128347	838 bp	mRNA	linear	EST 02-DEC-2003
DEFINITION	AGENCOURT_16696175 NIH_MGC_203 Mus musculus cDNA clone				
IMAGE	30790255 5', mRNA sequence.				
ACCESSION	CK128347				
VERSION	CK128347.1	GI:38618771			
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 838)				
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: <a href="mailto:cgabps@mail.nih.gov">cgabps@mail.nih.gov</a> Tissue Procurement: Naryan Bhat cDNA Library Preparation: Express Genomics cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: NDAMI107 row: d column: 08 High quality sequence stop: 717. Location/Qualifiers 1. .838 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="IMAGE:30790255" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH_MGC_203" /notes="Organ: placenta; Vector: pExpress-1; Site:1: EcorV; Site 2: NotI; RNA obtained from three placentas from female C57/BL6 mouse at 16 days pregnancy. Tissues were snap-frozen and kept at -80C for two days before RNA extraction and purification (Tri-reagent method). cDNA was primed using oligo-dT primer 5'-pGACTATTCATGCGAGCGCCGCC(7)25-3' and cloned into the EcorV/NotI sites of pExpress-1. Size-selection >1kb resulted in an average insert size of 1.3 kb. This primary, microquantity library is normalized to Cot5 (non-normalized primary library is NIH MGC 222) and was constructed by Express Genomics (Frederick, MD)."				
FEATURES					
source					

## ORIGIN

	Query Match.	96.4%;	Score 471.4;	DB 14;	Length 838;
	Best Local Similarity	99.2%;	Pred. No. 4.5e-131;		
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Qy	4	TGAGGCTAGATCTTCAGAACTGTTCCCTG-AGGATCCTGGTCCAAACTCTTTTACAGGCTT	62		
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Qy	63	ATACTGCTATTATCATAGACCTTCAGGCAAAATCTCTCAAGAGATGATTTGGCCAAACCT	122		
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Db	240	TCCGTGGTGTATCTCAGCTCAGACTCTGATACTACACAAGATGTTTCCCTGTCTCTGGAG	299		
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Qy	243	GGGACCTTTGCAATAGCACTGGGAAGCCCAAAATGTCTCTGAGAAGGATCTTTGTGCAT	302		
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 VERSION BC038338.1 GI:23398571  
 KEYWORDS HTC.  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 884)  
 Strausberg, R.  
 Direct Submission  
 Submitted (01-OCT-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapbs-x@mail.nih.gov](mailto:cgapbs-x@mail.nih.gov)  
 Tissue Procurement: Marcello Bento Soares, Ph.D.  
 cDNA Library Preparation: Soares Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
 Contact: [amadansystemsbiology.org](mailto:amadansystemsbiology.org)  
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha  
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting  
 Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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 QY 4 TGAGGCTAGATCTTCAGAACTGTTCCCTG-AGGATCCTGTCACAACTTTTACAGGCTT 62  
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 AK002276  
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 Mus musculus (house mouse)  
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 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning  
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 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
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 Normalization and subtraction of cap-trapper-selected cDNAs to  
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 Genome Res. 10 (10), 1617-1630 (2000)  
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 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
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 1  
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 High-efficiency full-length cDNA cloning  
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 Normalization and subtraction of cap-trapper-selected cDNAs to  
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 3  
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
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 RIKEN integrated sequence analysis (RISA) system--384-format  
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 RESULT 9  
 AK002276  
 LOCUS  
 DEFINITION  
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 VERSION  
 KEYWORDS HTG; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1  
 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning  
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 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
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 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
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 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,  
 Itoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsushita, S., Kawai, J.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
 20530913  
 11076861  
 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

AUTHORS 5

TITLE The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

JOURNAL Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

REFERENCE Nature 420, 563-573 (2002)

AUTHORS 6 (bases 1 to 933)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koyama, S., Kurahara, C., Matsuyama, I., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Yuramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute: 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'-GAGAGAGAGCGCGCACTCGAGTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGAGAGAGATCGAAGCTCAATTATTTATTAACCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.

Location/Qualifiers

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/dev\_stage="adult"

10. .681

/note="unnamed protein product; putative similar to APOPTOSIS RELATED PROTEIN APR-3 (Homo sapiens) [SPTR|Q9Y5L7, evidence: PASTY, 72.2%ID, 98.5%length, match=612]"

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RESULT 10

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LOCUS MP34905.f1 Barstead MPLRBI Mus musculus cDNA clone IMAGE:571160 5',

DEFINITION mRNA sequence.

ACCESSION AA108529

VERSION AA108529.1 GI:1660101

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 614)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE The WashU-HMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu



243 GGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTCTCAGAACGGATCTTTGTGCAT 302  
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 BE994240  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

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 Mus musculus (house mouse)  
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 Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Genome Res. 6 (9), 791-806 (1996)  
 97044477  
 8889548  
 Contact: Chin, H  
 National Institute of Mental Health  
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
 20892-9643, USA  
 Tel: 301 443 1706  
 Fax: 301 443 9890  
 Email: mEST@mail.nih.gov

Oligo-dt track not found, Not I site shown in beginning of sequence  
 is likely internal to the message. cDNA Library Preparation: M.B.  
 Soares Lab Clone distribution: Researchers may obtain BMAP cDNA  
 clones from RESEARCH GENETICS. It should be noted that Bento Soares  
 is generating a small number of additional specialized  
 non-redundant arrays of BMAP cDNAs whose availability will be  
 considered under appropriate and limited collaborative arrangements  
 The tissue for this library was contributed by Dr. Xin-Yuan Fu,  
 Yale University School of Medicine The following repetitive  
 elements were found in this cDNA sequence: 202-231,  
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 ultimately derived from mouse retina tissue libraries at

various stages of development. For a detailed description  
 of the library from which this clone was derived, please  
 visit our web site at brainest.eng.uiowa.edu. The tissue  
 for this library was contributed by Dr. Xin-Yuan Fu, Yale  
 University School of Medicine  
 TAG\_SEQ=None found"

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 Mus musculus (house mouse)

ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 635)  
 Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,  
 Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,  
 Fiddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,  
 Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,  
 Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,  
 Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,  
 Zhu,Q., Person,C. and Sands,A.T.  
 Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
 screen to identify potential targets for therapeutic intervention  
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
 Contact: Zambrowicz BP



OmniBank  
Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: materials@lexgen.com  
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
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VERSION BQ748981.1 GI:21895768  
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ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 720)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE  
JOURNAL  
COMMENT  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgspps-remail.nih.gov  
Tissue Procurement: Dr. James Lin, University of Iowa  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E.B. Consortium/LLNL at: <http://image.llnl.gov>  
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)  
The following repetitive elements were found in this cDNA sequence: 239-268, >RLTR5\_MM#LTR/Retroviral (matched complement)  
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/clone\_lib="NIH BMAP\_FBO"  
/note="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is TGAGAGACC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP). Gene Discovery in the Developing Mouse Nervous System", supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN  
Query Match 91.6%; Score 447.8; DB 13; Length 720;  
Best Local Similarity 99.1%; Pred. No. 5.7e-124;  
Matches 460; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
Qy 4 TGAGGCTAGATCTTCAGAACTGTTCCCTG-AGGATCTGTCACAACTTTTACAGGCTT 62  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 582709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/prodata/2/ina/6B\_COMB.seq: \*  
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6: /cgn2\_6/prodata/2/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	182.6	37.3	524	4	US-09-621-976-1403 Sequence 1403, Ap
2	165	33.7	498	4	US-09-621-976-2829 Sequence 2829, Ap
3	45.4	9.3	452	4	US-09-621-976-16474 Sequence 16474, A
4	34.4	7.0	474	4	US-09-621-976-18033 Sequence 18033, A
5	31.8	6.5	2196	4	US-09-540-236-124 Sequence 124, App
6	31.8	6.5	65792	4	US-09-596-002-31 Sequence 31, Appl
7	30.8	6.3	1515	4	US-09-134-000C-2080 Sequence 2080, Ap
8	30.4	6.2	1089	4	US-09-543-681A-895 Sequence 895, App
9	30.4	6.2	1725	4	US-09-543-681A-2148 Sequence 2148, Ap
10	30	6.1	374	3	US-08-638-931-48 Sequence 48, Appl
11	29.8	6.1	2859	4	US-09-328-352-425 Sequence 425, App
12	29.6	6.1	881	4	US-09-598-401C-22 Sequence 22, Appl
13	29.4	6.0	694	3	US-09-328-111-616 Sequence 616, App
14	29.4	6.0	832	4	US-09-621-976-2813 Sequence 2813, Ap
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16	29.4	6.0	7766	4	US-09-125-619-3 Sequence 3, Appl
17	29	5.9	442	4	US-09-227-357-132 Sequence 132, App
18	29	5.9	5837	1	US-07-686-340-1 Sequence 1, Appl
19	29	5.9	5837	1	US-08-004-1398-1 Sequence 1, Appl
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21	29	5.9	5837	1	US-08-271-364A-1 Sequence 1, Appl
22	29	5.9	5837	2	US-08-811-492-1 Sequence 1, Appl
23	29	5.9	5837	2	US-08-222-715B-1 Sequence 1, Appl
24	29	5.9	5837	5	PCT-US96-10545A-1 Sequence 1, Appl
25	29	5.9	64457	4	US-09-803-671B-3 Sequence 3, Appl
26	28.8	5.9	359	4	US-08-838-931-51 Sequence 51, Appl
27	28.6	5.8	3504	2	US-08-760-797A-2 Sequence 2, Appl

C 28	28.6	5.8	3504	2	US-08-760-797A-4	Sequence 4, Appl
C 29	28.6	5.8	3504	3	US-08-932-929B-2	Sequence 2, Appl
C 30	28.6	5.8	3504	3	US-08-932-929B-4	Sequence 4, Appl
C 31	28.4	5.8	1353	4	US-08-956-171B-521	Sequence 521, App
C 32	28.4	5.8	1695	4	US-09-142-623-12	Sequence 12, Appl
C 33	28.4	5.8	1809	4	US-09-508-264A-2	Sequence 2, Appl
C 34	28.4	5.8	1859	4	US-09-508-264A-7	Sequence 7, Appl
C 35	28.4	5.8	2560	5	PCT-US92-05707-1	Sequence 1, Appl
C 36	28.2	5.8	750	4	US-09-134-001C-514	Sequence 514, App
C 37	28.2	5.8	786	1	US-08-345-756-1	Sequence 1, Appl
C 38	28.2	5.8	786	1	US-08-625-198-1	Sequence 1, Appl
C 39	28.2	5.8	886	6	5219739-23	Patent No. 5219739
C 40	28.2	5.8	2039	1	US-08-345-756-5	Sequence 5, Appl
C 41	28.2	5.8	2039	1	US-08-625-198-5	Sequence 5, Appl
C 42	28.2	5.8	24183	3	US-08-943-731-3	Sequence 3, Appl
C 43	28	5.7	466	4	US-09-833-381-842	Sequence 842, App
C 44	28	5.7	2119	4	US-09-240-639-7	Sequence 7, Appl
C 45	28	5.7	5506	4	US-09-976-594-530	Sequence 530, App

## ALIGNMENTS

## RESULT 1

US-09-621-976-1403  
; Sequence 1403, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621.976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 1403  
; LENGTH: 524  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 10..504  
; NAME/KEY: sig\_peptide  
; LOCATION: 10..99  
; OTHER INFORMATION: Von Heijne matrix  
; OTHER INFORMATION: score 8.8000019073486  
; OTHER INFORMATION: seq ALLLALGVERALA/LP  
US-09-621-976-1403

Query Match 37.3%; Score 182.6; DB 4; Length 524;

Best Local Similarity	81.9%;	Pred. No. 2.3e-55;	Mismatches 50;	Indels 3;	Gaps 3;
Matches 245;	Conservative 1;				
QY	4	TCAGCTAGATCTTCAGAACTGTTCCTT-CAGGATCTCTGGTCCAACTTTTACAGGCTT	62		
DB	227	TGGGCTGGATCTCCAGAACTGTTCCTTCTGTGAGGACCTTGTCCAACTTTTCATCAGGCAC	286		
QY	63	ATAGTCTATATCATAGACCTTCAGCAATCTCTCAAGATGATTGGCCACACCT	122		
DB	287	ATACCACCTGTTCATAGACCTTGAAGCAACCCCTCAAAGGTGACTTGGCCACACCT	346		
QY	123	TCCGTGGTGTTCATCAGCTGTGACTCTGATACCAAGATGTTCCTGTCTGGAG	182		
DB	347	TCCGTGGTGTTCATCAGCTGTGACTCTGATACCAAGATGTTCCTGTGGAG	406		
QY	183	GTAGTAATGCTGGACAATTTACTTTTTCAGGACAAGAGATTTGCCAAGGGAAA	242		
DB	407	GAATTAATGCTGGAATACTATCCTCTTATATAGACACCAAACTCTGTCAA-GGCAAA	465		
QY	243	GGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTCTCTGAGAACGGATCTTTGTGCA	301		

Db 466 AGRACCTTTGCAATAACACTGG-GGACCAGAAATGTGTCTCTGAGAAATGGAATCTTGTGTA 523

## RESULT 2

```

US-09-621-976-2829
; Sequence 2829, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSEI.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2829
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 155..391
US-09-621-976-2829

```

Query Match	33.7%;	Score 165;	DB 4;	Length 498;
Best Local Similarity	87.2%;	Pred. No. 4.6e-49;		
Matches 191;	Conservative 0;	Mismatches 27;	Indels 1;	Gaps 1;
QY	272	GAATGTCTCTGAGAACGATCTTTGGCATCTGACGGTCTCTGGTCTTTTTCAGATGCCTT	331	
Db	152	GAATGTGTCTCTGAGATGGATCTTTGTTACCTCATGCTCCAGGTCTTTTGCAGTGTGTT	211	
QY	332	TGTCTGATGTTTCCATGGATCAAGTGAT - GAGCGAGGCTCATTTTCTACTGCTTAT	390	
Db	212	TGTCTGATGTTTCCATGGATCAAGTGATGGCGCCAGGGCTGGTCTCTACTGCTTAT	271	
QY	391	GTTCTTTGGGATTCTGGGATCCACACGCTAGCCATCTNCAATCTTACTTTGGGGAAACCCA	450	
Db	272	GTTCTTTGGGATTCTGGAGGCACCACTCTATCCGTCTCATTTGCTTTGGGGACACCCA	331	
QY	451	GGCGCGGAAGCCCAAGGCTTNTATGAGCCACACAAGACTTT	489	
Db	332	GGCGCGGAAGCCCAAGACTTTCATGACTAGATAGGCTTT	370	

### RESULTS

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US-09-621-976-16474
; Sequence 16474, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 16474
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-16474

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Query Match 9.3%; Score 45.4; DB 4; Length 452;  
Best Local Similarity 73.4%; Pred. No. 4.2e-06;  
Matches 58; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 4 TGAGGCTAGATCTTCAGAACTGTTCCCTGAGGATCCTGGTCCAAACTTTTACAGGCTTA 63

Db 374 TGGGGCTGGATCTCCAGAACTGTTCTCTGGAGGACCCCTGGTCAAACCTTCATCAGGCACA 433

Qy 64 TACTGCTATTATCATAGAC 82  
Db 434 TACCACTGTTCATCATAGAC 452

## RESULT 4

```

US-09-621-976-18033
; Sequence 18033, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 18033
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 16
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-18033

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Query Match	7.08	Score 34.4	DB 4	Length 474
Best Local Similarity	16.98	Pred. No. 0.039		
Matches 53	Conservative 115	Mismatches 146	Indels 0	Gaps 0
QY	49	CTTTTACAGCGCTTATAC	TGCTATTATCATAGACCTTC	CAGGCAAAATCCCTCTCAAGGATGA 108
Db	152	MWTTTMMRRRKKSGYRW	TGKKKKKTITWMA	ANCYTTTWRSTWMMRRRAAAKTYTCM 211
QY	109	TTTGCCCAACACCTTC	CGTGCGGTTTACTCAGCT	TGCAGACTTACCAACAAGATGT 168
Db	212	MSKTMCCWACC	CMCCVRRARS	CCMRSCHRSYTYNMCYYYYYYMWYKGRMYWWRGGMKKR 271
QY	169	TCCTCTGCTCTGGAGGT	AGTAAATGCCTGGAGCAATG	TATCTTCTTCAAGGACAACGACAT 228
Db	272	MYMYKKKSKMMG	SKMWKRAWWARKT	TYTWAYTYTYTKRMCCYMKRTCMMDMYSR 331

[illegible]

## RESULT, T 5

US-09-540-236-124/c  
Sequence 124, Application US/09540236  
Patent No. 6673910  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND  
TITLE OF INVENTION: FOR DIAGNOSTICS  
FILE REFERENCE: 2709-2005-001  
CURRENT APPLICATION NUMBER: US/09/54  
CURRENT FILING DATE: 2000-04-04  
NUMBER OF SEQ ID NOS: 3840  
SEQ ID NO 124

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; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2080
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2080

Query Match
Best Local Similarity 6.3%; Score 30.8; DB 4; Length 1515;
Matches 62; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 106 TGATTGGCCAAACACCTTCCTGGTGGTTTACTCAGCTGCAGACTCTGTATACCAAGA 165
Db 344 TGATTAGCAACAATTTTTCAGTTTCTCTGATTCTCGTTATTTCTTCTCAGCTACT 285

QY 166 TGTTCCTGCTGCTGGAGGTAGTAATGCTGGCAATGTTACTTCTTTCAAGGA 219
Db 284 TGTGCCAAGTAATGAAAGTCGTTCAATCTTTGAACTTTTCCTTATCTGATGA 231

RESULT 8
US-09-543-681A-895
; Sequence 895, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 895
; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-895

Query Match
Best Local Similarity 6.2%; Score 30.4; DB 4; Length 1089;
Matches 76; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 132 TTACTAGCTGCAGACTCTGTATACCAAGAGTGTTCCTGCTGGAGGTAGTAATG 191
Db 518 TTAATGAATTCCTATATAACACAGCAAGTTTGTTCATCTAATCCAGAAATTCGATG 577

QY 192 CCTGGCAATGTTACTTCTTCAAGGACAAGCAGATTTCGCAAGGCAAGGACCTTT 251
Db 578 CCGATATAAATTTGGTTTTTACGATGTTTTCATATAGTCATGGTTCATAGAAATTTT 637

QY 252 GCAATAGCACTGGAAGCCCAAGAAATGTCTCT 283
Db 638 CATATACCACAGAGGTTTTCGAACCTATCTCT 669

RESULT 9
US-09-543-681A-2148
; Sequence 2148, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
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; LENGTH: 2196
; TYPE: DNA
; ORGANISM: M.catarrhalis
US-09-540-236-124

Query Match
Best Local Similarity 6.5%; Score 31.8; DB 4; Length 2196;
Matches 75; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 205 TACTTCTTTCAAGGACAAGCAGATTTCGCAAGGCAAGGACCTTTGCAATAGCACTGG 264
Db 1795 TAATTCTTTGCTCGCTCAAGATGATAGATAATGTTAAATGTCTTGTGCCATGCTGAGT 1736

QY 265 AAGCCAGAAATGTGTCCTGAGAACGATCTGTGTCATCTGACGTCCTGGTCTTTTGA 324
Db 1735 GTTCGATGACAATGCAAGGATCAGATTGAGCAAAATGGGGTGTGCAATCAGATGCA 1676

QY 325 GTGCGTTTGTGCTGATGGTTTCATGG 351
Db 1675 ATGCGATTTCGGTGATTCATCGCGG 1649

RESULT 6
US-09-596-002-31
; Sequence 31, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.
; APPLICANT: Patterson, Chandra
; APPLICANT: Berg, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: PM-0008-4 US
; CURRENT APPLICATION NUMBER: US/09/596,002
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/140,121
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 31
; LENGTH: 65792
; TYPE: DNA
; ORGANISM: M. catarrhalis
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte template ID No. 6632636 31
; PUBLIC INFORMATION:
US-09-596-002-31

Query Match
Best Local Similarity 6.5%; Score 31.8; DB 4; Length 65792;
Matches 75; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 205 TACTTCTTTCAAGGACAAGCAGATTTCGCAAGGCAAGGACCTTTGCAATAGCACTGG 264
Db 53870 TAATTCTTTGCTCGCTCAAGATGATAGATAATGTTAAATGTCTTGTGCCATGCTGAGT 53929

QY 265 AAGCCAGAAATGTGTCCTGAGAACGATCTGTGTCATCTGACGTCCTGGTCTTTTGA 324
Db 53930 GTTCGATGACAATGCAAGGATCAGATTGAGCAAAATGGGGTGTGAAATCAGATGCA 53989

QY 325 GTGCGTTTGTGCTGATGGTTTCCATGG 351
Db 53990 ATGCGATTTCGGTGATTCATCGCGG 54016

RESULT 7
US-09-134-000C-2080/c
; Sequence 2080, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
```

; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 2148  
; LENGTH: 1725  
; TYPE: DNA  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-2148

Query Match 6.2%; Score 30.4; DB 4; Length 1725;  
Best Local Similarity 50.0%; Pred. No. 2.5; Mismatches 0; Indels 0; Gaps 0;  
Matches 76; Conservative 0

QY 132 TTACTGAGTGCAGACTGTATACCAAGATGTTCCCTGCTGGAGGTAGTAATG 191  
DB 101 TTAATGAATTCCTATATACCAAGAAATGTTGTCATCTAATCCAGAATTCGATG 160

QY 192 CTGGGACATGTTACTTCTTCAAGACAAAGCATGTTCCGAAAGGCAAGGACCTTT 251  
DB 161 CCGATATAAAATTTGGTTTACGATGATTTTCATATTAGTCATGTTCAATAGAATTTT 220

QY 252 GCAATAGCACTGGAAGCCCAAGATGTGCT 283  
DB 221 CATATACCAAGAGGTTTGCACTATCT 252

RESULT 10  
US-08-638-931-48  
; Sequence 48, Application US/08638931  
; Patent No. 6194145  
; GENERAL INFORMATION:  
; APPLICANT: HEIDRICH, Bj rn  
; APPLICANT: ROBINSON, Peter-Nicholas  
; APPLICANT: TIECKE, Frank  
; APPLICANT: ROLFS, Arndt  
; TITLE OF INVENTION: Genus and species-specific identification of  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP  
; STREET: 655 Fifteenth Street N.W. Suite 330  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-5701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/638,931  
; FILING DATE: 25-APR-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 195 15 891.1  
; FILING DATE: 29-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murray, Robert B.  
; REGISTRATION NUMBER: 22,980  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)638-5000  
; TELEFAX: (202)638-4810  
; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 374 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:

; ORGANISM: Legionella anisa  
; STRAIN: WA-316-C2  
; INDIVIDUAL ISOLATE: 24ani  
US-08-638-931-48

Query Match 6.1%; Score 30; DB 3; Length 374;  
Best Local Similarity 55.9%; Pred. No. 1.3;  
Matches 57; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 257 AGCACTGGAAGCCCAAGAAATGTCTGAGAACGATCTTGTGCATCTGACGGTCTCTGGT 316  
DB 63 AGGTGTGAAGCACAGTAATGTGTGAAGCTAACTTGTACTAATTGGCTGATTGCTTGAC 122

QY 317 CTTTTCAGTGGTGTGTGCTGATGGTTTCCATGATACAAAG 358  
DB 123 CATATACTAGTTACTTTCAGATTGTGATGCGAATACAAAG 164

RESULT 11  
US-09-328-352-425  
; Sequence 425, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 425  
; LENGTH: 2859  
; TYPE: DNA  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-425

Query Match 6.1%; Score 29.8; DB 4; Length 2859;  
Best Local Similarity 51.1%; Pred. No. 5.8;  
Matches 70; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 205 TACTCTTTCAGGACAAAGCATGTTCCCAAGGCAAGGACCTTTGCATACATGCG 264  
DB 744 TAATCATTTGCTCGAACAAAGGTTCCGGAAGGACATATGACCTCAATAAATGAATGA 803

QY 265 AAGCCCAAGAAATGTCTCTGAGAACGATCTTGTGCATCTGACGGTCTCTGCTCTTTTGCA 324  
DB 804 GAGGCTTGAAGCCATCATATATTAGCATTTGCATGAACAGAGGTATCCGACC 863

QY 325 GTGCGTTTGTGCTGATG 341  
DB 864 GTGGGATTGGGATATTG 880

RESULT 12  
US-09-598-401C-22  
; Sequence 22, Application US/09598401C  
; Patent No. 6596925  
; GENERAL INFORMATION:  
; APPLICANT: Perera, J. Ranjan  
; APPLICANT: Bagleton, Clare  
; APPLICANT: Rice, Stephen J.  
; TITLE OF INVENTION: Compositions and Methods for the  
; FILE REFERENCE: 11000.1036c2  
; CURRENT APPLICATION NUMBER: US/09/598,401C  
; CURRENT FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591  
; PRIOR FILING DATE: 1999-07-30  
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599  
; PRIOR FILING DATE: 1999-03-25  
; NUMBER OF SEQ ID NOS: 120

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 881
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-598-401C-22

Query Match          6.1%; Score 29.6; DB 4; Length 881;
Best Local Similarity 45.0%; Pred. No. 3.1;
Matches 56; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 319 TTTCAGCTGGTTGTCTGATGTTTCCAGTGATACAAGTGTATAGGCGAGGCTCATTT 378
Db 655 TTTTCGGTGGTTGTGTGTCTGTGTTTCCCTGTGTCAGAGGCTTATTAGAGGTCCTTTT 714

QY 379 TTCACCTCTTATGTTCTTTGGGATCTTGGGATCCACCACG 418
Db 715 GCCTTTTCCTAGTCTCTTTTGTCTTTGTTGTTTCCATG 754

RESULT 13
US-09-328-111-616
; Sequence 616, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CDD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 616
; LENGTH: 694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(694)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-616

Query Match          6.0%; Score 29.4; DB 3; Length 694;
Best Local Similarity 46.9%; Pred. No. 3.1;
Matches 69; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 23 CTGTTCCCTGAGGATCCCGTGCCAAACCTTTTACAGGCTTATACGTGTTATCATAGAC 82
Db 424 CTGACCCCTTGCAANNCCGTGGGCATACCTTGGAAATGGTTCGCCCTTCCATTTTGGCAAGC 483

QY 83 CTTCAGGCAAAATCTCTCAAGATGATTGGCCAAACACTTCCGTGGGTTTACTCAGCTG 142
Db 484 CTTTAAACCGGNTTTTTCAGAAATCTAGTCGNNAAAAACCTTCTCTTTTANGGAATN 543

QY 143 CAGACTCTGTACTACCAACAAGATTT 169
Db 544 GANATTNGAAANCCCCCAANGGAATTT 570

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Best Local Similarity 55.3%; Pred. No. 15;  
 Matches 57; Conservative 0; Mismatches 46; Indels 0; Gaps 0;  
 Qy 17 TCAGAACGTGTTCCCTGAGGATCCTGGTCCAAACTTTTACAGGCTTATAGTCTATTATC 76  
 Db 3418 TCAGATGCTATGCGATTGATCCGTTCAAGATGCTTTAAATGGGATATTTTAAATAC 3477  
 Qy 77 ATAGACCTTCAGGCAAAATCCTCTCAAGGATGATTGGCCAACA 119  
 Db 3478 ACCAAGATCAAGTAGTCTCTCAATGATCTTCTGCAAAAAA 3520

Search completed: June 25, 2004, 22:19:11  
 Job time : 65 secs



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OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 22:05:51 ; Search time 318 Seconds  
(without alignments)  
7044.505 Million cell updates/sec

Title: US-09-773-476-294

Perfect score: 489  
Sequence: 1 gactgagctgattcttcag.....tntatgagccacacagactt 489

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	353	72.2	932	13	US-10-245-752-7
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4	353	72.2	932	14	US-10-245-859-7
5	353	72.2	932	15	US-10-001-054-1
6	353	72.2	932	15	US-10-245-103-7
7	353	72.2	932	15	US-10-245-107-7
8	353	72.2	932	15	US-10-245-143-7
9	353	72.2	932	15	US-10-245-771-7
10	353	72.2	932	15	US-10-245-851-7
11	353	72.2	932	15	US-10-245-883-7
12	353	72.2	932	15	US-10-237-535-7
13	353	72.2	932	15	US-10-238-183-7
14	353	72.2	932	15	US-10-238-283-7
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16	353	72.2	932	15	US-10-245-147-7	Sequence 7, Appli
17	353	72.2	932	15	US-10-245-730-7	Sequence 7, Appli
18	353	72.2	932	15	US-10-245-739-7	Sequence 7, Appli
19	353	72.2	932	15	US-10-246-210-7	Sequence 7, Appli
20	353	72.2	932	15	US-10-239-196-7	Sequence 7, Appli
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22	353	72.2	932	15	US-10-243-409-7	Sequence 7, Appli
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25	353	72.2	932	15	US-10-245-033-7	Sequence 7, Appli
26	353	72.2	932	15	US-10-243-095-7	Sequence 7, Appli
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29	353	72.2	932	15	US-10-245-473-7	Sequence 7, Appli
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33	353	72.2	932	15	US-10-243-320-7	Sequence 7, Appli
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#### ALIGNMENTS

#### RESULT 1

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; Sequence 1, Application US/09726348  
; Patent No. US2002025553A1  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Ying-Fei  
; APPLICANT: et al,  
; TITLE OF INVENTION: Transforming Growth Factor Alpha HIII  
; FILE REFERENCE: PF220P1  
; CURRENT APPLICATION NUMBER: US/09/726,348  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: 08/778,545  
; PRIOR FILING DATE: 1997-01-03  
; PRIOR APPLICATION NUMBER: 60/011,136  
; PRIOR FILING DATE: 1996-01-04  
; PRIOR APPLICATION NUMBER: 60/168,387  
; PRIOR FILING DATE: 1999-12-02  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 923  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-726-348-1

Query Match 72.2%; Score 353; DB 9; Length 923;  
Best Local Similarity 84.0%; Pred. No. 2.5e-114;  
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

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PRIOR APPLICATION NUMBER: 10/197942  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
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PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
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PRIOR APPLICATION NUMBER: 60/090689  
PRIOR FILING DATE: 1998-08-25  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 116  
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LENGTH: 932  
TYPE: DNA  
ORGANISM: Homo Sapien  
FEATURE:  
NAME/KEY: unsure  
LOCATION: 911  
OTHER INFORMATION: unknown base  
US-10-245-859-7

Query Match 72.2%; Score 353; DB 13; Length 932;  
Best Local Similarity 84.0%; Pred. No. 2.5e-114; Mismatches 0; Gaps 1;  
Matches 409; Conservative 77; Indels 1;  
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349 TCCGTGGTCTTACTCAGCTGCAGACTCTGATCTACTACCAAGATGTTCCCTGCTCTGAG 408  
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409 GAATTAATGCTCGGAATCTATCACTCTTATATAGAACCAAAATCTGTCAGGGCAA 468  
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RESULT 4  
US-10-001-054-1  
Sequence 1, Application US/10001054  
Publication No. US20020192209A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Baker, Kevin  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin  
APPLICANT: Hebert, Carolyn  
APPLICANT: Hensel, William  
APPLICANT: Kabakoff, Rhona  
APPLICANT: Shelton, David  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC  
FILE OF INVENTION: CELL GROWTH  
FILE REFERENCE: P3034R1PCT  
CURRENT APPLICATION NUMBER: US/10/001,054  
CURRENT FILING DATE: 2001-11-30  
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PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
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PRIOR FILING DATE: 1998-04-24  
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PRIOR FILING DATE: 2000-02-11  
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PRIOR FILING DATE: 2001-03-01  
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PRIOR FILING DATE: 2001-05-25  
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PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: PCT/US01/21735  
PRIOR FILING DATE: 2001-07-09  
PRIOR APPLICATION NUMBER: PCT/US01/27099  
PRIOR FILING DATE: 2001-08-29  
NUMBER OF SEQ ID NOS: 91  
SEQ ID NO 1  
LENGTH: 932  
TYPE: DNA  
ORGANISM: Homo Sapien  
FEATURE:  
NAME/KEY: unsure  
LOCATION: 911  
OTHER INFORMATION: unknown base

Query Match 72.2%; Score 153; DB 14; Length 932;  
Best Local Similarity 84.0%; Pred. No. 2.5e-114; Indels 1; Gaps 1;  
Matches 409; Conservative 0; Mismatches 77;

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Db 229 TGGGCTGGATCTCCAGAACTGTTCTCTGGAGGACCTGTTCCAACTTTTACAGGAC 288  
QY 63 ATACTGCTATTATCATAGACCTTCAGGCAATCTCTCAAGGATGATTTCGCCAACACCT 122  
Db 289 ATACCACTGTTCATAGACCTTCGAAGCAACCCCTCAAGGATGATTTCGCCAACACCT 348  
QY 123 TCCGTGGGTTTACTCAGCTGCAGACTCTGATCTACTACCAAGATGTTCCCTGTCTCTGGAG 182  
Db 349 TCCGTGGGTTTACTCAGCTGCAGACTCTGATCTACTACCAAGATGTTCCCTGTCTCTGGAG 408

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QY 183 GTAGTAATGCTGGGACAAATGTTACTTTTCAAGCAAGCAGATTTGCCAAGGGCAA 242
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QY 303 CTGACGGCTCTGCTTTTGGAGTGGTGTGCTGATGTTTCCATGGATACAAAGTGT 362
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QY 423 CCATCTNCATTTACTTTGGGAAACCCAGCGCGGAAAGCCAAAGCTTTCATGAGCCAC 482
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QY 483 AAGACTT 489
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; Publication No. US20030068778A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C112
; CURRENT APPLICATION NUMBER: US/10/245,103
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
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; PRIOR FILING DATE: 1998-06-25
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; TYPE: DNA
; ORGANISM: Homo Sapien
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: 911
; OTHER INFORMATION: unknown base
US-10-245-103-7

Query Match 72.2%; Score 353; DB 15; Length 932;
Best Local Similarity 84.0%; Pred. No. 2.5e-114;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

QY 4 TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCCTGGTCCAAAATTTTTCACAGGCTT 62
Db 229 TGGGGCTGGATCTCCAGAACTGTTCTCTGGAGAACCTTGTCTCCAAAATTTTCATCAGGCAC 288
QY 63 ATACTGCTATTATCATAGACCTTCAGGCAAAATCCTCTCAAGAGATGATTTGGCCAAACACT 122
Db 289 ATACCACCTGTCATAGACCTTCAGGCAAAATCCTCTCAAGAGATGATTTGGCCAAACACT 348
QY 123 TCCGTGGTCTTACTCAGCTGCAGACTCTGATACCTACCAAGATGTTCCCTGTCTCTGGAG 182
Db 349 TCCGTGGTCTTACTCAGCTGCAGACTCTGATACCTACCAAGATGTTCCCTGTCTCTGGAG 408
QY 183 GTAGTAATGCTGGGACAAATGTTACTTTTCAAGGACCAAGCAGATTTGCCAAGGGCAA 242
Db 409 GAAATTAATGCTGGGAACTATACCTCTTATATAGCAACCAAACTGTCAAGGGCAA 468
QY 243 GGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTCCTGAGAACGGATCTTGCGAT 302
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QY 363 TGAGCAGGGCTCAATTTCACTGCTTATGTTCTTTGGGATCTGGGATCCACCGCTAG 422
Db 589 TCGGCAGGGCTCGTTCTCACTGCTTATGTTCTTTGGGATCTGGGATCCACCGCTAT 648
QY 423 CCATCTNCATTTACTTTGGGAAACCCAGCGCGGAAAGCCAAAGCTTTCATGAGCCAC 482
Db 649 CCGTCTCCATTTCTGTTGGGCGACCCAGCGCGGAAAGCCAAAGCTTTCATGAGCCAC 708
QY 483 AAGACTT 489
Db 709 AGGTCTT 715

RESULT 6
US-10-245-107-7
; Sequence 7, Application US/10245107
; Publication No. US20030068779A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C71
; CURRENT APPLICATION NUMBER: US/10/245,107
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
```

;; PRIOR APPLICATION NUMBER: 60/063046  
;; PRIOR FILING DATE: 1997-10-24  
;; PRIOR APPLICATION NUMBER: 60/065027  
;; PRIOR FILING DATE: 1997-11-10  
;; PRIOR APPLICATION NUMBER: 60/079689  
;; PRIOR FILING DATE: 1998-03-27  
;; PRIOR APPLICATION NUMBER: 60/086478  
;; PRIOR FILING DATE: 1998-05-22  
;; PRIOR APPLICATION NUMBER: 60/087607  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/089801  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/090557  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090689  
;; PRIOR FILING DATE: 1998-06-25  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 116  
;; SEQ ID NO 7  
;; LENGTH: 932  
;; TYPE: DNA  
;; ORGANISM: Homo Sapien  
;; FEATURE:  
;; NAME/KEY: unsure  
;; LOCATION: 911  
;; OTHER INFORMATION: unknown base  
US-10-245-107-7

Query Match 72.2%; Score 353; DB 15; Length 932;  
Best Local Similarity 84.0%; Pred. No. 2.5e-114;  
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;  
  
QY 4 TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCCTGTCACAACTTTTACAGGCTT 62  
DB 229 TGGGCTGGATCTCCAGAACTGTTCTCTGAGGACCTGTCACAACTTTCATCAGGCAC 288  
QY 63 ATACTGCTATTATCATAGACTTCAGCAAACTCTCAAGATGATGTTGGCCCAACCT 122  
DB 289 ATACCACTGTCTATAGACTTCAGCAAACTCTCAAGGTCGACTTGGCCCAACCT 348  
QY 123 TCGTGCGTTTACTCAGCTCAGACTCTGATCTACCAAGATGTTCCCTGCTGGAG 182  
DB 349 TCGTGCGTTTACTCAGCTCAGACTCTGATCTACCAAGATGTTCCCTGCTGGAG 408  
QY 183 GTAGTAATGCTGGGCAATGTTACTTCTTCAAGGACAGAGATTTGCCAAGGCCAAA 242  
DB 409 GAATTAATGCTGGAATACTATCACCTCTTATATAGACCAACAACTCTGTCAGGGCAAA 468  
QY 243 GGGACCTTTCGAATAGACTTCAGGACCCAGAAATGTTCTGAGACGGATCTTGTCAT 302  
DB 469 AGAACCTTTCGAATAACACTGCGGACCCAGAAATGTTCTGAGATGGATCTTGTCAT 528  
QY 303 CTGACGCTCTGCTCTTTTTCAGTGCGTTTGTCTGATGTTTCCATGGATACAAGTGA 362  
DB 529 CTGATGCTCAGGCTCTTTTCAGTGCGTTTGTCTGATGTTTCCATGGATACAAGTGA 588  
QY 363 TGAGGAGGCTCATTTTCTACTGTTTCTTCTGATGTTTCTGATGTTTCCATGGATACAAGTGA 422  
DB 589 TGGCCAGGCTCGTCTCTACTGTTTCTTCTGATGTTTCTGATGTTTCCATGGATACAAGTGA 648  
QY 423 CCATCTNCATCTTACTTTTGGGGAACCCAGCGCCGAAAGCCAGAGCTTTCATGAGCCACAC 482  
DB 649 CCGTCTCCATCTGCTTTTGGGACCCAGCGCCGAAAGCCAGAGCTTTCATGACTACTAT 708  
QY 483 AAGACTT 489  
DB 709 AGGTCTT 715

RESULT 7  
US-10-245-143-7  
; Sequence 7, Application US/10245143  
; Publication No. US20030068780A1

;; GENERAL INFORMATION:  
;; APPLICANT: Baker, Kevin  
;; APPLICANT: Eaton, Dan  
;; APPLICANT: Filvaroff, Ellen  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin  
;; APPLICANT: Smith, Victoria  
;; APPLICANT: Stephan, Jean-Phillippe  
;; APPLICANT: Watanabe, Colin  
;; APPLICANT: Wood, William  
;; APPLICANT: Zhang, Zemin  
;; APPLICANT: Fong, Sherman  
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
;; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
;; FILE REFERENCE: P3630R1C90  
;; CURRENT APPLICATION NUMBER: US/10/245,143  
;; CURRENT FILING DATE: 2002-09-16  
;; PRIOR APPLICATION NUMBER: 10/197942  
;; PRIOR FILING DATE: 2002-07-18  
;; PRIOR APPLICATION NUMBER: 60/059114  
;; PRIOR FILING DATE: 1997-09-17  
;; PRIOR APPLICATION NUMBER: 60/063046  
;; PRIOR FILING DATE: 1997-10-24  
;; PRIOR APPLICATION NUMBER: 60/065027  
;; PRIOR FILING DATE: 1997-11-10  
;; PRIOR APPLICATION NUMBER: 60/079689  
;; PRIOR FILING DATE: 1998-03-27  
;; PRIOR APPLICATION NUMBER: 60/086478  
;; PRIOR FILING DATE: 1998-05-22  
;; PRIOR APPLICATION NUMBER: 60/087607  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/089801  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/090557  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090689  
;; PRIOR FILING DATE: 1998-06-25  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 116  
;; SEQ ID NO 7  
;; LENGTH: 932  
;; TYPE: DNA  
;; ORGANISM: Homo Sapien  
;; FEATURE:  
;; NAME/KEY: unsure  
;; LOCATION: 911  
;; OTHER INFORMATION: unknown base  
US-10-245-143-7

Query Match 72.2%; Score 353; DB 15; Length 932;  
Best Local Similarity 84.0%; Pred. No. 2.5e-114;  
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;  
  
QY 4 TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCCTGTCACAACTTTTACAGGCTT 62  
DB 229 TGGGCTGGATCTCCAGAACTGTTCTCTGAGGACCTGTCACAACTTTCATCAGGCAC 288  
QY 63 ATACTGCTATTATCATAGACTTCAGCAAACTCTCAAGATGATGTTGGCCCAACCT 122  
DB 289 ATACCACTGTCTATAGACTTCAGCAAACTCTCAAGGTCGACTTGGCCCAACCT 348  
QY 123 TCGTGCGTTTACTCAGCTCAGACTCTGATCTACCAAGATGTTCCCTGCTGGAG 182  
DB 349 TCGTGCGTTTACTCAGCTCAGACTCTGATCTACCAAGATGTTCCCTGCTGGAG 408  
QY 183 GTAGTAATGCTGGGCAATGTTACTTCTTTCAGGACAGAGATTTGCCAAGGCCAAA 242  
DB 409 GAATTAATGCTGGAATACTATCACCTCTTATATAGACCAACAACTCTGTCAGGGCAAA 468  
QY 243 GGGACCTTTCGAATAGACTTCAGGACCCAGAAATGTTCTGAGACGGATCTTGTCAT 302  
DB 469 AGAACCTTTCGAATAACACTGCGGACCCAGAAATGTTCTGAGATGGATCTTGTCAT 528

QY 303 CTGACGGCTCGGCTTTTTCAGTGGCTTTGCTGTGATGGTTTCCATGATACAAAGTGTA 362  
Db 529 CTGATGGTCCAGGCTTTTTCAGTGGCTTTGCTGTGATGGTTTCCATGATACAAAGTGTA 588  
QY 363 TGAGCAGGGCTCATTTCACCTGCTTATGTTCTTTTGGGATCTGGGATCCACCAAGCTAG 422  
Db 589 TCGCCAGGGCTCGTCTCAGTCTTATGTTCTTTTGGGATCTGGGATCCACCAAGCTAG 648  
QY 423 CCATCTNCATTCTACTTTGGGAAACCCAGCGCCGGAAGCCAAAGCTTATGAGCCACAC 482  
Db 649 CGGTCTCCATTCTGCTTTGGGCGCCAGCGCCGGAAGCCAAAGCTTATGAGCCACAC 708  
QY 483 AAGACTT 489  
Db 709 AGGTCTT 715

## RESULT 8

US-10-245-771-7  
; Sequence 7, Application US/10245771  
; Publication No. US20030068781A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C98  
; CURRENT APPLICATION NUMBER: US/10/245,771  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 7  
; LENGTH: 932  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 911  
; OTHER INFORMATION: unknown base  
US-10-245-771-7

Query Match

72.2%; Score 353; DB 15; Length 932;

Best Local Similarity 84.0%; Pred. No. 2.5e-114;  
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;  
QY 4 TGAGGCTAGATCTTCAGAACTGTTCCTT-CAGGATCCTGGTCCAAACTTTTACAGGCTT 62  
Db 229 TGGGGCTGGATCTCCAGAACTGTTCCTCTGGAGACCTGTCTCCAAACTTTTCACTAGGAC 288  
QY 63 ATACTGCTATTATCATAGACCTTCAGGCAATCCTCTCAAGGATGATTTGGCCCAACACCT 122  
Db 289 ATACCACTGTCAATCATAGACCTTCAGGCAATCCTCTCAAGGATGATTTGGCCCAACACCT 348  
QY 123 TCGTGGGTTTACTCAGCTGCAGACTCTGATACCTACCAAGATGTTCCCTGCTGGAG 182  
Db 349 TCGTGGCTTTACTCAGCTGCAGACTCTGATACCTACCAAGATGTTCCCTGCTGGAG 408  
QY 183 GTAGTATGCTGGGCAATGTTACTTCTTTCAAGGACAGCAGATTTGCCAGGGGCAA 242  
Db 409 GAATTAATGCTGGAATACCTATCACCTCTTATATAGAACCAAACTGTGCAAGGGGCAA 468  
QY 243 GGGACCTTTGCAATAGCAGCTGGAAGCCAGAAATGTCTCTGAGAACGGATCTTGTGCAT 302  
Db 469 AGAACCTTTGCAATAGCAGCTGGAAGCCAGAAATGTCTCTGAGAACGGATCTTGTGTAC 528  
QY 303 CTGACGGTCTCTGCTTTTTCAGTGGGTTTGTCTGATGGTTTCCATGGATCAAGTGTA 362  
Db 529 CTGATGGTCCAGGCTCTTTTTCAGTGGGTTTGTCTGATGGTTTCCATGGATCAAGTGTA 588  
QY 363 TGAGGAGGGCTCATTTTTCAGTGGGTTTGTCTGATGGTTTCCATGGATCAAGTGTA 422  
Db 589 TCGCCAGGGCTCGTCTCAGTGGGTTTGTCTGATGGTTTCCATGGATCAAGTGTA 648  
QY 423 CCATCTNCATTCTACTTTGGGAAACCCAGCGCCGGAAGCCAAAGCTTATGAGCCACAC 482  
Db 649 CGGTCTCCATTCTGCTTTGGGCGCCAGCGCCGGAAGCCAAAGCTTATGAGCCACAC 708  
QY 483 AAGACTT 489  
Db 709 AGGTCTT 715

## RESULT 9

US-10-245-851-7  
; Sequence 7, Application US/10245851  
; Publication No. US20030068782A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C93  
; CURRENT APPLICATION NUMBER: US/10/245,851  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478

; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 7  
; LENGTH: 932  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 911  
; OTHER INFORMATION: unknown base  
US-10-245-851-7

Query Match 72.2%; Score 353; DB 15; Length 932;  
Best Local Similarity 84.0%; Pred. No. 2.5e-114;  
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;  
QY 4 TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCTGTCCTCAAACTTTTACAGGCTT 62  
DB 229 TGGGCTGGATCTCCAGAACTGTTCTCTGGAGACCTGTCTCAAACTTTCATCAGGCAC 288  
QY 63 ATACTGCTATTATCATAGACCTTCAGGCAAACTCTCTCAAGGATGATTTGGCCAAACCT 122  
DB 289 ATACCCTGTCTCATATAGACCTTCAGGCAAACTCTCTCAAGGATGATTTGGCCAAACCT 348  
QY 123 TCCGTGGGTTTACTCAGTCTGAGACTCTGATCTTACCAAGATGTTCCCTGCTGGAG 182  
DB 349 TCCGTGGGTTTACTCAGTCTGAGACTCTGATCTTACCAAGATGTTCCCTGCTGGAG 408  
QY 183 CTAGTAATGCTGGCAAACTGTTTACTCTTTCAGGATCTGTCCTGAGACGATCTTGTGCAT 302  
DB 349 TCCGTGGGTTTACTCAGTCTGAGACTCTGATCTTACCAAGATGTTCCCTGCTGGAG 408  
QY 183 GTAGTAATGCTGGCAAACTGTTTACTCTTTCAGGATCTGTCCTGAGACGATTTGCCAAGGCAAA 242  
DB 409 GAATTAATGCTGGATCTCCAGAACTGTTCTCTGGAGACCTGTCTCAAACTTTCATCAGGCAC 468  
QY 243 GGGACCTTTGCAATAGACCTTCAGGCAAACTCTCTCAAGGATGATTTGGCCAAACCT 302  
DB 469 AGAACCTTTGCAATAGACCTTCAGGCAAACTCTCTCAAGGATGATTTGGCCAAACCT 468  
QY 303 CTGACGGTCTCTGCTTTTTCAGTGGGTTTGTCTGATGTTTCCATGGATGATTTGGCCAAACCT 422  
DB 529 CTGATGCTCCAGGCTCTTTCAGTGGGTTTGTCTGATGTTTCCATGGATGATTTGGCCAAACCT 588  
QY 363 TGAGGAGGGCTCATTTTCTACTGTTTGTCTGATGTTTCCATGGATGATTTGGCCAAACCT 422  
DB 589 TGGCCAGGGCTCTGTTCTACTGTTTGTCTGATGTTTCCATGGATGATTTGGCCAAACCT 648  
QY 423 CCATCTNCAITCTACTTTTGGGAAACCCAGCGCCGAAAGCCAGGCTTTCATGAGCCACAC 482  
DB 649 CCGTCTCCATCTCTGTTTGGGAAACCCAGCGCCGAAAGCCAGGCTTTCATGAGCTACAT 708  
QY 483 AAGACTT 489  
DB 709 AGGCTTT 715

RESULT 10  
US-10-245-883-7  
; Sequence 7, Application US/10245883  
; Publication No. US20030068783A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Fillaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin

; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3830R1C70  
; CURRENT APPLICATION NUMBER: US/10/245.883  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 7  
; LENGTH: 932  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 911  
; OTHER INFORMATION: unknown base  
US-10-245-883-7

Query Match 72.2%; Score 353; DB 15; Length 932;  
Best Local Similarity 84.0%; Pred. No. 2.5e-114;  
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;  
QY 4 TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCTGTCCTCAAACTTTTACAGGCTT 62  
DB 229 TGGGCTGGATCTCCAGAACTGTTCTCTGGAGACCTGTCTCAAACTTTCATCAGGCAC 288  
QY 63 ATACTGCTATTATCATAGACCTTCAGGCAAACTCTCTCAAGGATGATTTGGCCAAACCT 122  
DB 289 ATACCCTGTCTCATATAGACCTTCAGGCAAACTCTCTCAAGGATGATTTGGCCAAACCT 348  
QY 123 TCCGTGGGTTTACTCAGTCTGAGACTCTGATCTTACCAAGATGTTCCCTGCTGGAG 182  
DB 349 TCCGTGGGTTTACTCAGTCTGAGACTCTGATCTTACCAAGATGTTCCCTGCTGGAG 408  
QY 183 CTAGTAATGCTGGCAAACTGTTTACTCTTTCAGGATCTGTCCTGAGACGATTTGCCAAGGCAAA 242  
DB 409 GAATTAATGCTGGATCTCCAGAACTGTTCTCTGGAGACCTGTCTCAAACTTTCATCAGGCAC 468  
QY 243 GGGACCTTTGCAATAGACCTTCAGGCAAACTCTCTCAAGGATGATTTGGCCAAACCT 302  
DB 469 AGAACCTTTGCAATAGACCTTCAGGCAAACTCTCTCAAGGATGATTTGGCCAAACCT 468  
QY 303 CTGACGGTCTCTGCTTTTTCAGTGGGTTTGTCTGATGTTTCCATGGATGATTTGGCCAAACCT 362  
DB 529 CTGATGCTCCAGGCTCTTTCAGTGGGTTTGTCTGATGTTTCCATGGATGATTTGGCCAAACCT 588  
QY 363 TGAGGAGGGCTCATTTTCTACTGTTTGTCTGATGTTTCCATGGATGATTTGGCCAAACCT 422



Db 589 TCGCGCAGGCTCGTTCTCACTGTTATGTTCTTCGGGATTCCTGGAGCCACCTCTAT 648  
QY 423 CCATCTNATCTACTTTGGGAAACCCAGCGCGGAAAGCCAAAGCTTATGAGCCAC 482  
Db 649 CGGTCTCCATCTGTTTGGGCGACCCAGCGCGGAAAGCCAAAGCTTATGAGCTACAT 708  
QY 483 AAGACTT 489  
Db 709 AGGTCTT 715

RESULT 11  
US-10-237-535-7  
; Sequence 7, Application US/10237535  
; Publication No. US20030073188A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C3  
; CURRENT APPLICATION NUMBER: US/10/237,535  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: 60/091358  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/099803  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/106932  
; PRIOR FILING DATE: 1998-11-03  
; PRIOR APPLICATION NUMBER: 60/115554  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/119342  
; PRIOR FILING DATE: 1999-02-09  
; PRIOR APPLICATION NUMBER: 60/123957  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123972  
; PRIOR FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: 60/127372  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/131271  
; PRIOR FILING DATE: 1999-04-27  
; PRIOR APPLICATION NUMBER: 60/133459  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/135725  
; PRIOR FILING DATE: 1999-05-25  
; PRIOR APPLICATION NUMBER: 60/135729  
; PRIOR FILING DATE: 1999-05-25  
; PRIOR APPLICATION NUMBER: 60/135750  
; PRIOR FILING DATE: 1999-05-25  
; PRIOR APPLICATION NUMBER: 60/138385  
; PRIOR FILING DATE: 1999-06-09  
; PRIOR APPLICATION NUMBER: 60/140653  
; PRIOR FILING DATE: 1999-06-22  
; PRIOR APPLICATION NUMBER: 60/141037  
; PRIOR FILING DATE: 1999-06-23  
; PRIOR APPLICATION NUMBER: 60/144732  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 60/144758  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 60/144790  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 60/145228  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 60/145698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: 60/146222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: 60/146843  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: 60/148188  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: 60/148513  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 60/149327  
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; PRIOR FILING DATE: 1999-08-20  
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; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: 60/151734  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: 60/162506  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: 60/170262  
; PRIOR FILING DATE: 1999-12-09  
; PRIOR APPLICATION NUMBER: 60/177118  
; PRIOR FILING DATE: 2000-01-20  
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; PRIOR FILING DATE: 2000-02-02  
; PRIOR APPLICATION NUMBER: 60/180921  
; PRIOR FILING DATE: 2000-02-08  
; PRIOR APPLICATION NUMBER: 60/187202  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: 60/198587  
; PRIOR FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: 60/199614  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 60/206330  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/206368  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/209832  
; PRIOR FILING DATE: 2000-06-05  
; PRIOR APPLICATION NUMBER: 60/218371  
; PRIOR FILING DATE: 2000-07-13  
; PRIOR APPLICATION NUMBER: 60/222695  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: 60/229896  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/230621  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/232887

Query Match 72.2%; Score 353; DB 15; Length 932;  
Best Local Similarity 84.0%; Pred. No. 2.5e-114;  
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;  
4 TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCTGCTCCAAACTTTTACAGGCTT 62

PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: 60/235147  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: 60/261878  
PRIOR FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: 60/261910  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 60/261939  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 60/262150  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: 60/264395  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 60/286421  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 60/267623  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/274399  
PRIOR FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: 60/280982  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/282129  
PRIOR FILING DATE: 2001-04-04  
PRIOR APPLICATION NUMBER: 60/282199  
PRIOR FILING DATE: 2001-04-04  
PRIOR APPLICATION NUMBER: 60/290589  
PRIOR FILING DATE: 2001-05-09  
PRIOR APPLICATION NUMBER: 09/180997  
PRIOR FILING DATE: 1998-11-19  
PRIOR APPLICATION NUMBER: 09/267213  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 09/380137  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/380138  
PRIOR FILING DATE: 1999-08-25  
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PRIOR FILING DATE: 1999-10-18  
PRIOR APPLICATION NUMBER: 09/423741  
PRIOR FILING DATE: 1999-11-10  
PRIOR APPLICATION NUMBER: 09/709238  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 09/802706  
PRIOR FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: 09/872035  
PRIOR FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 09/924419  
PRIOR FILING DATE: 2001-08-06  
PRIOR APPLICATION NUMBER: 09/927796  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 09/929404  
PRIOR FILING DATE: 2001-08-13  
PRIOR APPLICATION NUMBER: 09/931836  
PRIOR FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: 09/941992  
PRIOR FILING DATE: 2001-08-28  
PRIOR APPLICATION NUMBER: 09/946374  
PRIOR FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 10/001054  
PRIOR FILING DATE: 2001-11-30  
PRIOR APPLICATION NUMBER: 10/052586  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 10/081056  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: 10/119480  
PRIOR FILING DATE: 2002-04-09

Db 229 TGGGCTGGATCTCCAGAACTGTTCTCTGGAGGACCCCTGGTCCAAACTTTTCATCAGGCAC 288  
QY 63 ATACTGCTATTATCATAGACCTTCAGGCAATCTCTCAAGGATGATTGGCCCAACCT 122  
Db 289 ATACCACTGTCAATAGACCTGCAAGCAAAACCCCTCAAGGTGACTTTGGCCCAACCT 348  
QY 123 TCCGTGGGTTTACTCAGCTGCAGACTCTGATPACTACCAAGATGTTCCCTGTCTCTGGAG 182  
Db 349 TCCGTGGGTTTACTCAGCTCCAGACTCTGATPACTGCCCCAACATGTCAACTGTCTCTGGAG 408  
QY 183 GTAGTAATGCCCTGGGACAATGTTACTTCTTTCAAGGACCAAGCAATTTGCCAAGGGCAAA 242  
Db 409 GAATTAATGCCCTGGAATACTATCACCTCTTATATAGACAACCAATCTGTCAAGGGCAAA 468  
QY 243 GGGACCTTTGCAATAGCACTGGAAAGCCAGAAATGTGTCTCTGAGAACGGATCTTTGTGCAT 302  
Db 469 AGAACCTTTGCAATAGCACTGGGAGCCAGAAATGTGTCTCTGAGATGGATCTTTGTGTAC 528  
QY 303 CTGACGTCCTGGTCTTTTTCAGTGGGTTTGTGCTGATGTTTCCATGGATACAAAGTGA 362  
Db 529 CTGATGGTCCAGGCTTTTTCAGTGGGTTTGTGCTGATGTTTCCATGGATACAAAGTGA 588  
QY 363 TGAGGACGGGCTCAATTTTCACTGCTTATGTTCTTTGGATCTGGATCCACCAAGCTAG 422  
Db 589 TGGCCAGGGCTCGTCTCACTGCTTATGTTCTTTGGATCTGGATCCACCAAGCTAG 648  
QY 423 CCATCTNCAATCTACTTTGGGAAACCCAGGCCCCGAAAGCCAAAGCTTATGAGCCACAC 482  
Db 649 CCGTCTCCATCTGCTTTGGGCGACCCAGGCCCCGAAAGCCAAAGCTTATGAGCTACAT 708  
QY 483 AAGACTT 489  
Db 709 AGGCTT 715

RESULT 12  
US-10-238-183-7  
Sequence 7, Application US/10238183  
Publication No. US20030073189A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Eaton, Dan  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Phillippe  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
APPLICANT: Fong, Sherman  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3630R1C11  
CURRENT APPLICATION NUMBER: US/10/238,183  
CURRENT FILING DATE: 2002-09-09  
PRIOR APPLICATION NUMBER: 10/197942  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801

, PRIOR FILING DATE: 1998-06-18  
, PRIOR APPLICATION NUMBER: 60/090557  
, PRIOR FILING DATE: 1998-06-24  
, PRIOR APPLICATION NUMBER: 60/090689  
, PRIOR FILING DATE: 1998-06-25  
, PRIOR APPLICATION NUMBER: 60/091358  
, PRIOR FILING DATE: 1998-07-01  
, PRIOR APPLICATION NUMBER: 60/091978  
, PRIOR FILING DATE: 1998-07-07  
, PRIOR APPLICATION NUMBER: 60/099803  
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, PRIOR APPLICATION NUMBER: 60/115554  
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, PRIOR APPLICATION NUMBER: 60/119342  
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, PRIOR FILING DATE: 1999-03-11  
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, PRIOR FILING DATE: 1999-04-27  
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, PRIOR FILING DATE: 1999-08-17  
, PRIOR APPLICATION NUMBER: 60/149395  
, PRIOR FILING DATE: 1999-08-17  
, PRIOR APPLICATION NUMBER: 60/150114  
, PRIOR FILING DATE: 1999-08-20  
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, PRIOR FILING DATE: 1999-08-31  
, PRIOR APPLICATION NUMBER: 60/151734  
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, PRIOR APPLICATION NUMBER: 60/177118  
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, PRIOR FILING DATE: 2000-02-02  
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, PRIOR FILING DATE: 2000-02-08  
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, PRIOR FILING DATE: 2000-03-03  
, PRIOR APPLICATION NUMBER: 60/198587  
, PRIOR FILING DATE: 2000-04-18  
, PRIOR APPLICATION NUMBER: 60/199614  
, PRIOR FILING DATE: 2000-04-25  
, PRIOR APPLICATION NUMBER: 60/206330  
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, PRIOR APPLICATION NUMBER: 60/209832  
, PRIOR FILING DATE: 2000-06-05  
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, PRIOR FILING DATE: 2000-08-02  
, PRIOR APPLICATION NUMBER: 60/229896  
, PRIOR FILING DATE: 2000-09-01  
, PRIOR APPLICATION NUMBER: 60/230621  
, PRIOR FILING DATE: 2000-09-05  
, PRIOR APPLICATION NUMBER: 60/232887  
, PRIOR FILING DATE: 2000-09-15  
, PRIOR APPLICATION NUMBER: 60/235147  
, PRIOR FILING DATE: 2000-09-22  
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, PRIOR FILING DATE: 2001-01-12  
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, PRIOR FILING DATE: 2001-02-09  
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, PRIOR FILING DATE: 2001-03-09  
, PRIOR APPLICATION NUMBER: 09/872035  
, PRIOR FILING DATE: 2001-06-01  
, PRIOR APPLICATION NUMBER: 09/918585  
, PRIOR FILING DATE: 2001-07-30  
, PRIOR APPLICATION NUMBER: 09/924419

; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: 09/927796  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/929404  
; PRIOR FILING DATE: 2001-08-13  
; PRIOR APPLICATION NUMBER: 09/931836  
; PRIOR FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: 09/941992  
; PRIOR FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 09/946374  
; PRIOR FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: 10/001054  
; PRIOR FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 10/081056  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: 10/119480  
; PRIOR FILING DATE: 2002-04-09

Query Match 72.2%; Score 353; DB 15; Length 932;  
Best Local Similarity 84.0%; Pred. No. 2.5e-114;  
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;  
QY 4 TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCTGTGTCACAACTTTTACAGGCTT 62  
DB 229 TGGGGCTGGATCTCCAGAACTGTTCTCTGGAGACCCCTGTGTCACAACTTTTATCAGGCAC 288  
QY 63 ATACTGCTATTATCATAGACTTCAGCAAACTCTCTCAAGGATGATTTGGCCAAACACT 122  
DB 289 ATACCATGTCATCATAGACTTCAGCAAACTCTCTCAAGGATGATTTGGCCAAACACT 348  
QY 123 TCCGTGGGTTTACTCAGCTCGAGACTCTGATCTACTTACCAAGATGTTCCCTGTCTCGAG 182  
DB 349 TCCGTGGGTTTACTCAGCTCGAGACTCTGATCTACTTACCAAGATGTTCCCTGTCTCGAG 408  
QY 183 GTAGTAATGCTGGGACAAATGTTACTTCTTTCAGGCAAGCAGATTTGCCAGGGGCAAA 242  
DB 409 GAATTAATGCTGGGACAAATGTTACTTCTTTCAGGCAAGCAGATTTGCCAGGGGCAAA 468  
QY 243 GGGACCTTTGCAATAGCACTTCAGCAAACTCTCTCAAGGATGATTTGGCCAAACACT 302  
DB 469 AGAACCTTTGCAATAGCACTTCAGCAAACTCTCTCAAGGATGATTTGGCCAAACACT 528  
QY 303 CTGACGGTCTGTGTTTTCAGTGGGTTTGTCTGATGTTTCCATGGATACAAAGTGA 362  
DB 529 CTGATGCTCCAGGTCCTTTTTCAGTGGGTTTGTCTGATGTTTCCATGGATACAAAGTGA 588  
QY 363 TGAGGCAAGGCTCATTTTTCAGTGGGTTTGTCTGATGTTTCCATGGATACAAAGTGA 422  
DB 589 TGAGGCAAGGCTCATTTTTCAGTGGGTTTGTCTGATGTTTCCATGGATACAAAGTGA 548  
QY 423 CCATCTNCAATTCATTTTTCAGTGGGTTTGTCTGATGTTTCCATGGATACAAAGTGA 482  
DB 649 CCGTCTCCATTTCTGTTTTCAGTGGGTTTGTCTGATGTTTCCATGGATACAAAGTGA 708  
QY 483 AAGACTT 489  
DB 709 AGTCTTT 715

RESULT 13  
US-10-238-283-7  
; Sequence 7, Application US/10238283  
; Publication No. US20030073190A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Baton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria

; APPLICANT: Stephan, Jean-Philippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P363031C.5  
; CURRENT APPLICATION NUMBER: US/10/238,283  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 7  
; LENGTH: 932  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 911  
; OTHER INFORMATION: unknown base  
; US-10-238-283-7

Query Match 72.2%; Score 353; DB 15; Length 932;  
Best Local Similarity 84.0%; Pred. No. 2.5e-114;  
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;  
QY 4 TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCTGTGTCACAACTTTTACAGGCTT 62  
DB 229 TGGGGCTGGATCTCCAGAACTGTTCTCTGGAGACCCCTGTGTCACAACTTTTATCAGGCAC 288  
QY 63 ATACTGCTATTATCATAGACTTCAGCAAACTCTCTCAAGGATGATTTGGCCAAACACT 122  
DB 289 ATACCATGTCATCATAGACTTCAGCAAACTCTCTCAAGGATGATTTGGCCAAACACT 348  
QY 123 TCCGTGGGTTTACTCAGCTCGAGACTCTGATCTACTTACCAAGATGTTCCCTGTCTCGAG 182  
DB 349 TCCGTGGGTTTACTCAGCTCGAGACTCTGATCTACTTACCAAGATGTTCCCTGTCTCGAG 408  
QY 183 GTAGTAATGCTGGGACAAATGTTACTTCTTTCAGGCAAGCAGATTTGCCAGGGGCAAA 242  
DB 409 GAATTAATGCTGGGACAAATGTTACTTCTTTCAGGCAAGCAGATTTGCCAGGGGCAAA 468  
QY 243 GGGACCTTTGCAATAGCACTTCAGCAAACTCTCTCAAGGATGATTTGGCCAAACACT 302  
DB 469 AGAACCTTTGCAATAGCACTTCAGCAAACTCTCTCAAGGATGATTTGGCCAAACACT 528  
QY 303 CTGACGGTCTGTGTTTTCAGTGGGTTTGTCTGATGTTTCCATGGATACAAAGTGA 362  
DB 529 CTGATGCTCCAGGTCCTTTTTCAGTGGGTTTGTCTGATGTTTCCATGGATACAAAGTGA 588  
QY 363 TGAGGCAAGGCTCATTTTTCAGTGGGTTTGTCTGATGTTTCCATGGATACCAAGCTAG 422  
DB 589 TGAGGCAAGGCTCATTTTTCAGTGGGTTTGTCTGATGTTTCCATGGATACCAAGCTAG 648

QY 423 CCATCTNCATTCTACTTTGGGGAACCCAGCGCCGGAAGCCAGGCTTATGAGCCAC 482  
DB 649 CCGTCTCCATTCTGTTTGGGGAACCCAGCGCCGGAAGCCAGGCTTATGAGCCAC 708  
QY 483 AAGACTT 489  
DB 709 AGGTCTT 715

RESULT 14  
US-10-238-370-7  
; Sequence 7, Application US/10238370  
; Publication No. US20030073192A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Baton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3630R1C10  
; CURRENT APPLICATION NUMBER: US/10/238,370  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 7  
; LENGTH: 932  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 911  
; OTHER INFORMATION: unknown base  
US-10-238-370-7

Query Match 72.2%; Score 353; DB 15; Length 932;  
Best Local Similarity 84.0%; Pred. No. 2.5e-114;  
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

QY 4 TGAGGCTAGACTTTCAGACTTTCCT-GAGATCCTGGTCCAACTTTTACAGGCTT 62  
DB 229 TGGGGCTGAGCTTCAGACTTTCCTGGAGGACCCCTGGTCCAACTTTTACAGGAC 288  
QY 63 ATACTGCTATTATCATAGACCTTCAGGCAATCTCTCAAGGATGATTGGCCACACT 122

DB 289 ATACCACCTGTCATCATAGACCTTGAAGCAAAACCCCTCAAGGTGACTTTGGCCAAACCT 348  
QY 123 TCCTGTGGTGTACTCTAGCTGCAGACTCTGATATACCAAGATGTTCCCTGTCTGGAG 182  
DB 349 TCGTGGCTTTACTAGCTCCAGACTCTGATCTGCCACAACATGTCACACTGCTGGAG 408  
QY 183 GTAGTAATGCTGGGACAATGTTACTTCTTCAAGGACAGCAGATTTGCCAAGGGGAAA 242  
DB 409 GAATTAATGCTGGAATACTATCACCTCTTATATAGACCAACCAATCTGTCAGGGGAAA 468  
QY 243 GGGACCTTTGCAATAGCACTGGAAAGCCAGAAATGTCTCTGAGAACGGATCTTGTSCAT 302  
DB 469 AGAACCTTTGCAATAGCACTGGGAGCCAGAAATGTCTCTGAGAAATGATCTTGTGTAC 528  
QY 303 CTGACGGTCTCTGCTTTTTCAGTGGCTTGTCTGATGTTTCCATGGATACAAGTGA 362  
DB 529 CTGATGCTCCAGGCTCTTTTGCAGTGTGTGTCTGATGTTTCCATGGATACAAGTGA 588  
QY 363 TGAGGACAGGCTCATTTTCACTGCTTATGTTCTTGGGATTTCTGGATCCACACGCTAG 422  
DB 589 TGGCCAGGCTGCTTCTCACTGCTTATGTTCTTGGGATTTCTGGATCCACACGCTAT 648  
QY 423 CCATCTNCATTCTACTTTGGGAAACCCAGCGCCGGAAGCCAGGCTTATGAGCCAC 482  
DB 649 CCGTCTCCATTCTGTTTGGGGAACCCAGCGCCGGAAGCCAGGCTTATGAGCCAC 708  
QY 483 AAGACTT 489  
DB 709 AGGTCTT 715

RESULT 15  
US-10-245-055-7  
; Sequence 7, Application US/10245055  
; Publication No. US20030073192A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Baton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3630R1C88  
; CURRENT APPLICATION NUMBER: US/10/245,055  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689

; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116

; SEQ ID NO 7

; LENGTH: 932

; TYPE: DNA

; ORGANISM: Homo Sapien

; FEATURES:

; NAME/KEY: unsure

; LOCATION: 911

; OTHER INFORMATION: unknown base

US-10-245-055-7

Query Match 72.2%; Score 353; DB 15; Length 932;  
Best Local Similarity 84.0%; Pred. No. 2.5e-114;  
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;  
Qy 4 TGAGGCTAGATCTTCAGAACTGTTCCCT-CAGGATCCTGGTCCAAACTTTTACAGGCTT 62  
Db 229 TGGGCTGGATCTCCAGAACTGTTCTCTGGAGACCTGGTCCAAACTTTCATCAGGCAC 288  
Qy 63 ATACTGCTATATCATAGACTTCAGGCAAACTCTCTCAGGATGATTTGGCCAAACACT 122  
Db 289 ATACCACTGTCACTAGACCTGCAAGCAAAACCCCTCAAAGGTGACTTGGCCAAACACT 348  
Qy 123 TCCGTGGGTTTACTCAGCTCAGACTCTGATCTTACCACAAGATGTTCCCTGTCTGGAG 182  
Db 349 TCCGTGGCTTTACTCAGCTCAGACTCTGATCTTACCACAAGATGTTCCCTGTCTGGAG 408  
Qy 183 GTAGTAATGCTGGGCAATGTTACTTTTCAAGGACAGCAGATTTCAGGCAAA 242  
Db 409 GAATTAATGCTGGGCAATGTTACTTTTCAAGGACAGCAGATTTCAGGCAAA 468  
Qy 243 GGGACCTTTGCAATAGCACTGGAAGCCGCAAAATGTTCTCTGAGACGGATCTTGTGCAT 302  
Db 469 AGAACCTTTGCAATAGCACTGGAAGCCGCAAAATGTTCTCTGAGATGGATCTTGTGTAC 528  
Qy 303 CTGACGCTCCTGGTCTTTTTCAGTGGCTTTTGTCTGATGTTTCCATGGATCAAGTGA 362  
Db 529 CTGATGCTCCAGGCTTTTTCAGTGGCTTTTGTCTGATGTTTCCATGGATCAAGTGA 588  
Qy 363 TGAGGCAAGGCTCATTTTCTAGCTGTTATGTTCTTTGGGATCTGGGATCCACACCTAG 422  
Db 589 TGGCCAGGCTGCTTCTCAGTCTTATGTTCTTCGGGATCTGGGATCCACACCTAT 648  
Qy 423 CCATCTNCAITCTACTTTGGGAAACCCAGCGCCGGAAGCCAAAGGCTTATGAGCCACAC 482  
Db 649 CCGTCTCCATCTGCTTTGGGCAAGCCAGCGCCGGAAGCCAAAGGCTTATGAGCCACAC 708  
Qy 483 AAGACTT 489  
Db 709 AGTCTT 715

Search completed: June 25, 2004, 23:37:51  
Job time : 320 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 25, 2004, 09:08:52 ; Search time 54 Seconds  
(without alignments)  
5117.249 Million cell updates/sec

Title: US-09-773-476-294

Perfect score: 888  
Sequence: 1 gactgagctagattcttag.....tntatgacacacaagactt 489

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 3172214

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame\_n2p\_model -DEV=xlp  
-Q/cgn2\_1/USPTO.spool\_P/US09773476/runat\_25062004\_090846\_5808/app\_query.fasta\_1.647  
-DB=A\_Geneseq\_25Jan04 -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NCM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09773476 -CCN\_1\_181 -runat\_25062004\_090846\_5808 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6  
-FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A\_Geneseq\_29Jan04.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	690	77.7	229	2 AAW27087	Aaw27087 Human tra
2	690	77.7	229	2 AAY05282	Aay05282 EGF-like
3	690	77.7	229	2 AAY13944	Aay13944 Human tra
4	690	77.7	229	3 AAB33419	Aab33419 Human PRO
5	690	77.7	229	3 AAY88570	Aay88570 Human PRO
6	690	77.7	229	3 AAB50951	Aab50951 Human PRO
7	690	77.7	229	4 AAU04295	Aau04295 Transform
8	690	77.7	229	4 AAB20112	Aab20112 Human imm
9	690	77.7	229	4 AAB68595	Aab68595 PRO240_4
10	690	77.7	229	5 AAM51083	Aam51083 Human tra

11	690	77.7	229	5 ABG34033	ABg34033 Human PRO
12	690	77.7	229	6 ABU71417	ABu71417 Human neo
13	690	77.7	229	6 ADA01276	ADa01276 Human PRO
14	690	77.7	229	6 ADA43705	ADa43705 Human sec
15	690	77.7	229	6 ADA43473	ADa43473 Human sec
16	690	77.7	229	6 ADA01148	ADa01148 Human PRO
17	690	77.7	229	7 ADA01032	ADa01032 Human sec
18	690	77.7	229	7 ADA43589	ADa43589 Human sec
19	690	77.7	229	7 ADA06851	ADa06851 Human PRO
20	690	77.7	229	7 ADA08339	ADa08339 Novel hum
21	690	77.7	229	7 ADB99632	ADb99632 Human PRO
22	690	77.7	229	7 ADB86915	ADb86915 Human PRO
23	690	77.7	229	7 ADB66070	ADb66070 Human sec
24	690	77.7	229	7 ADB99748	ADb99748 Human PRO
25	690	77.7	229	7 ADB99403	ADb99403 Novel hum
26	690	77.7	229	7 ADB65954	ADb65954 Human sec
27	690	77.7	229	7 ADC23352	ADc23352 Human tra
28	690	77.7	229	7 ADC26045	ADc26045 Human PRO
29	690	77.7	229	7 ADE04872	ADe04872 Human PRO
30	690	77.7	229	7 ADE11178	ADe11178 Human PRO
31	690	77.7	229	7 ADD88109	ADd88109 Human PRO
32	690	77.7	229	7 ADD95404	ADd95404 Human sec
33	690	77.7	229	7 ADE06334	ADe06334 Human PRO
34	690	77.7	229	7 ADE38109	ADe38109 Human PRO
35	690	77.7	229	7 ADD88225	ADd88225 Human PRO
36	690	77.7	229	7 ADD90806	ADd90806 Human sec
37	690	77.7	229	8 ADE51659	ADe51659 Human sec
38	690	77.7	229	8 ADE51775	ADe51775 Human sec
39	690	77.7	229	8 ADE37633	ADe37633 Human sec
40	690	77.7	229	8 ADE37517	ADe37517 Human sec
41	690	77.7	229	8 ADD95288	ADd95288 Human sec
42	690	77.7	229	8 ADE37988	ADe37988 Human PRO
43	690	77.7	229	8 ADE76077	ADe76077 Human PRO
44	690	77.7	229	8 ADE39400	ADe39400 Human PRO
45	690	77.7	229	8 ADE04204	ADe04204 Human PRO

ALIGNMENTS

RESULT 1  
AAW27087  
ID AAW27087 standard; protein; 229 AA.

- XX AC AAW27087;
- XX DT 28-JAN-1998 (first entry)
- XX DE Human transforming growth factor alpha HIII.
- XX KW human transforming growth factor; TGF; TGF-alpha-HIII; angiogenesis; embryogenesis; ocular disorder; kidney disorder; liver disorder; neuronal disorder; alopecia; inflammation.
- XX OS Homo sapiens.

XX	Key	Location/Qualifiers
FT	Region	1..177
FT	Peptide	/label= soluble_portion_of_protein
FT		1..25
FT		/label= signal_peptide
FT		/note= "putative"
FT	Protein	26..229
FT		/label= mature_protein
FT	Region	126..177
FT		/label= active_site
FT	Region	178..204
FT		/label= transmembrane_portion
FT		/note= "putative"

WO9725349-A1.  
17-JUL-1997.

PF 04-JAN-1996; 96WO-US000149.  
 XX  
 PR 04-JAN-1996; 96WO-US000149.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Wei Y;  
 XX  
 DR WPI: 1997-372817/34.  
 DR N-PSDB; AAT85082.  
 XX  
 PT New human transforming growth factor-alpha homologue - used for  
 PT developing products for treating e.g. neurological disorders, kidney and  
 PT liver disorders, tumours, wounds, hair loss or skin disorders.  
 XX  
 PS Claim 15; Page 47; 63pp; English.  
 CC This protein has been putatively identified as a human transforming  
 CC growth factor (TGF) alpha analogue, TGF-alpha-HIII. The protein can  
 CC stimulate angiogenesis, embryogenesis, cell differentiation and function.  
 CC It can be used for therapeutic purposes for restoration or enhancement of  
 CC neurological functions diminished as a result of trauma or other damaging  
 CC pathologies such as AIDS dementia and senile dementia, to treat ocular  
 CC disorders, e.g. corneal inflammation, to destroy target cells, to treat  
 CC tumours, kidney or liver disorders or to treat wounds, burns or ulcers.  
 CC The polypeptide can also be used in the modulation of angiogenesis, bone  
 CC resorption, immune response, and synaptic and neuronal effector  
 CC functions, or the arachidonic acid cascade. It can also be used in  
 CC applications related to terminal differentiation e.g. in  
 CC hyperproliferative disorders such as inflammation or psoriasis and for  
 CC alopecia, hair loss or other skin conditions which affect hair follicular  
 CC development. Antagonists to TGF-alpha-HIII can be used for treating  
 CC tumours or skin disorders such as psoriasis. The products can also be  
 CC used for diagnosis and detection of the above disorders  
 XX  
 SQ Sequence 229 AA;  
 Alignment Scores:  
 Pred. NO.: 4.61e-63 Length: 229  
 Score: 690.00 Matches: 128  
 Percent Similarity: 89.68% Conservative: 11  
 Best Local Similarity: 82.58% Mismatches: 16  
 Query Match: 77.70% Indels: 1  
 Gaps: 2  
 DB: 0

US-09-773-476-294 (1-489) x AAW27087 (1-229)

QY 3 CTGAGGCTAGATCTTCAGAACTGTCCT-GAGGATCTGCTCCAACTTTTACAGGCT 61  
 DB 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92  
 QY 62 TATACTGCTATATCATAGACCTTCAGGCAAACTCTCTCAAGATGATTGGCCACACC 121  
 DB 93 HisThrThrValIleIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112  
 QY 122 TTCGCTGGGTTTACTAGCTCAGACCTGATATCTACCAAGATGTCCTCTCTGGA 181  
 DB 113 PheArgGlyPheThrGlnLeuGlnThrLeuLeuLeuLeuProGlnHisValAsnCysProGly 132  
 QY 182 GGTAGTAACTGGGCAATGTTTACTTCTTTCAAGGACCAAGCAGATTGCCAAGGGCAA 241  
 DB 133 GlyIleAsnAlaTrpAsnThrIleThr-SerTyrIleAspAsnGlnIleCysGlnGlyGln 152  
 QY 242 AGGACCTTTCATAGCAGCTGGAGCCGAGATGTCCTGAGACGGATCTTGCA 301  
 DB 153 LysAsnLeuCysAsnAsnThrThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172  
 QY 302 TCTCAGCGTCTCGTCTTTTTCAGTGGGTTGTCTGCTGATGTTTCCATGATCAAGTGT 361  
 DB 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys 192  
 QY 362 ATGAGGCGGCTCATTTTCTACTGCTATGTTCTTTTGGATTCTGGGATCCACCGCTA 421

DB 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212  
 QY 422 GCCATCTNCATCTTACTTTGGGAGCCAGCCGCGGAAGCCAAAG 466  
 DB 213 SerValSerIleLeuLeuLeuTrpAlaThrGlnArgGlyAlaLys 227  
 RESULT 2  
 AAY05282  
 ID AAY05282 standard; protein; 229 AA.  
 XX  
 AC AAY05282;  
 XX  
 DT 22-JUN-1999 (first entry)  
 XX  
 DE EGF-like homologue PRO240.  
 XX  
 KW Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246;  
 KW EBAF-2; inhibitor; tumour growth; cancer; EGF-like homologue;  
 KW FGF-8 homologue.  
 OS Homo sapiens.  
 XX  
 PN WO9914327-A2.  
 XX  
 PD 25-MAR-1999.  
 XX  
 PF 10-SEP-1998; 98WO-US018824.  
 XX  
 PR 17-SEP-1997; 97US-0059114P.  
 PR 17-SEP-1997; 97US-0059117P.  
 PR 18-SEP-1997; 97US-0059263P.  
 PR 15-OCT-1997; 97US-0062125P.  
 PR 17-OCT-1997; 97US-0062285P.  
 PR 17-OCT-1997; 97US-0062287P.  
 PR 24-OCT-1997; 97US-0062816P.  
 PR 29-OCT-1997; 97US-0063704P.  
 PR 25-NOV-1997; 97US-0066840P.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 PI Botstein D, Goddard A, Gurney A, Hillian X, Lawrence DA, Roy M;  
 PI Wood WI;  
 XX  
 DR WPI: 1999-229532/19.  
 DR N-PSDB; AAX28432.  
 XX  
 PT Antibodies against specific proteins overexpressed in tumors.  
 XX  
 PS Example 1; Fig 12; 130pp; English.  
 XX  
 CC This sequence represents the EGF-like homologue PRO240. The invention  
 CC relates to antibodies (Ab) that bind to any of the polypeptides (I)  
 CC designated PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246  
 CC or EBAF-2. The Ab, or other agents that inhibit expression and/or  
 CC activity of (I) are used: (i) to inhibit growth of tumours; and (ii) as  
 CC diagnostic/prognostic reagents for detection or quantification of (I) in  
 CC cells or tissues, by standard immunoassays, with overexpression being  
 CC indicative of cancer. For therapeutic use, the Ab may be conjugated to a  
 CC toxin, chemotherapeutic agent or radioisotope. Genes expressing (I), many  
 CC of which are growth factor homologues, are overexpressed in some cases of  
 CC cancer  
 XX  
 SQ Sequence 229 AA;  
 Alignment Scores:  
 Pred. NO.: 4.61e-63 Length: 229  
 Score: 690.00 Matches: 128  
 Percent Similarity: 89.68% Conservative: 11  
 Best Local Similarity: 82.58% Mismatches: 16  
 Query Match: 77.70% Indels: 1  
 Gaps: 2  
 DB: 0

US-09-773-476-294 (1-489) x AAY05282 (1-229)





autoimmune thrombocytopaenia; immune-mediated renal disease;  
 CC denvyelinating disease; hepatobiliary disease; Whipple's disease;  
 CC inflammatory bowel disease; gluten-sensitive enteropathy;  
 CC autoimmune disease; immune-mediated skin disease; allergic disease;  
 CC immunological disease; transplantation associated disease;  
 CC graft rejection; graft-versus-host-disease.

OS Homo sapiens.

XX WO200053758-A2.

XX 14-SEP-2000.

XX 02-MAR-2000; 2000WO-US005841.

PR 08-MAR-1999; 99WO-US005028.  
 PR 10-MAR-1999; 99US-0123618P.  
 PR 12-MAR-1999; 99US-0123957P.  
 PR 23-MAR-1999; 99US-0125775P.  
 PR 12-APR-1999; 99US-0128849P.  
 PR 20-APR-1999; 99WO-US008615.  
 PR 28-APR-1999; 99US-0131445P.  
 PR 04-MAY-1999; 99US-0132371P.  
 PR 14-MAY-1999; 99US-0134287P.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 28-JUL-1999; 99US-0146222P.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 08-SEP-1999; 99WO-US020394.  
 PR 13-SEP-1999; 99WO-US020944.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 05-OCT-1999; 99WO-US023089.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 29-NOV-1999; 99WO-US028214.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 30-NOV-1999; 99WO-US028409.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 02-DEC-1999; 99WO-US028564.  
 PR 02-DEC-1999; 99WO-US028565.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030999.  
 PR 30-DEC-1999; 99WO-US031274.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000277.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 18-FEB-2000; 2000WO-US004342.  
 PR 22-FEB-2000; 2000WO-US004414.

(GETH ) GENENTECH INC.

XX Askenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
 FI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
 FI Stewart TA, Tunas D, Watanabe CK, Wood WI, Yan M;

DR WPI; 2000-572271/53.

DR N-PSDB; AAC58584.

XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

XX Claim 33; Fig 12; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for

CC treating and diagnosing immune related disorders. The disorders are  
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central and  
 CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel  
 CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune  
 CC or immune-mediated skin diseases, allergic diseases, immunological  
 CC diseases of the lung, and transplantation associated diseases including  
 CC graft rejection and graft-versus-host-disease. AAC58578  
 CC represent PCR primers and hybridisation probes used in the isolation of  
 CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477  
 CC represent human PRO polynucleotide and protein sequences given in the  
 CC exemplification of the present invention

XX Sequence 229 AA;

XX Alignment Scores:

Pred. No.:	4,61e-63	Length:	229
Score:	690.00	Matches:	128
Percent Similarity:	89.68%	Conservative:	11
Best Local Similarity:	82.58%	Mismatches:	16
Query Match:	77.70%	Indels:	1
DB:	3	Gaps:	0

US-09-773-476-294 (1-489) x AAB33419 (1-229)

QY	3	CTGAGGCTAGATCTTCAGAACTGTTCCCT-CAGGATCCTGGTCCAACTTTTACAGGCT	61
DB	73	LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPhHisGlnAla	92
QY	62	TATACGTCTATTATCATAGACCTTCAGGCAATCTCTCAAGGATGATTTGGCCAAACC	121
DB	93	HisThrThrValIleLeuAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr	112
QY	122	TTCCGTGGTGTACTCAGCTCAGACTCTGATCTACAGAGATGTTCCCTGCTCTGGA	181
DB	113	PheArgGlyPheThrGlnLeuGlnThrLeuLeuLeuProGlnHisValAsnCysProGly	132
QY	182	GGTAGTAATGCTGGGCAATGTTACTTCTTCAAGGACACAGCAGATTTGCCAAGGCAA	241
DB	133	GlyIleAsnAlaTrpAsnThrIleThrSerTyrIleAspAsnGlnIleCysGlnGlyGln	152
QY	242	AGGACCTTTGCATAGCAGCTGGAGCCAGAAATGTCTCTGAGACCGATCTTGTCGA	301
DB	153	LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal	172
QY	302	TCTGACGCTCTGGTCTTTTCAGTGGCTTTGTCTGATGTTTCCATGGATCAAGTGT	361
DB	173	ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys	192
QY	362	ATGAGCGAGGCTCATTTTTCATCTGTTATGTTCTTGGGATCTGGGATCCACCGCTA	421
DB	193	MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu	212
QY	422	GCCATCTNCATCTTACTTTGGGACCCAGCGCGGAAGCCAAAG	466
DB	213	SerValSerIleLeuLeuTrpAlaThrGlnArgLysAlaLys	227

RESULT 5

AA58570

ID AAY88570 standard; protein; 229 AA.

XX AAY88570;

XX 09-AUG-2000 (first entry)

XX Human PRO240 amino acid sequence.

XX Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246;  
 KW PRO317; tumour growth inhibitor; cancer; diagnosis; treatment; human;



XX PS Claim 31; Fig 2; 188pp; English.

XX CC The present sequence is one of twenty eight novel P50 polypeptides. The

XX CC PRO polypeptides and their agonists, including antibodies, peptides, and

XX CC small molecule agonists, may be used to treat various tumours, e.g.,

XX CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal

XX CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,

XX CC central nervous system cancer, melanoma or leukaemia. They are also

XX CC useful for treating other disorders such as neuronal, glial, astrocytal,

XX CC hypothalamic and other glandular, macrophagal, epithelial, stromal and

XX CC biastocolic disorders, and inflammatory, angiogenic and immunological

XX CC disorders

XX SQ Sequence 229 AA;

Alignment Scores:

Pred. No.:	4.61e-63	Length:	229
Score:	690.00	Matches:	128
Percent Similarity:	89.68%	Conservative:	11
Best Local Similarity:	82.58%	Mismatches:	16
Query Match:	77.70%	Indels:	1
DB:	4	Gaps:	0

US-09-773-476-294 (1-489) x AAB50951 (1-229)

QY 3 CTGAGGCTAGACTTTCAGACTGTTCCCT-GAGGATCTGCTCCAAACTTTTACAGGCT 61

Db 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92

QY 62 TATACTGCTTATTATCATAGACCTTCAGCAAACTCTCAAGGATGTTGGCCACACC 121

Db 93 HisThrThrValIlelleAspLeuGlnAlaAsnProLeuGlyAspLeuAlaAsnThr 112

QY 122 TTCGGTGGTTACTCAGCTCAGACTCTGATACCTACCAAGATGTTCCCTGCTCTGGA 181

Db 113 PheArgGlyPheThrGlnLeuGlnThrLeuIleLeuProGlnHisValAsnCysProGly 132

QY 182 GGTAGTATCCCTGGCAATGTTACTCTTTCAAGGACAGAGATTTGCCAAGGCCAA 241

Db 133 GlyIleAsnAlaTrpAsnThrIleThrSerTyrlleAspAsnGlnIleCysGlnGlyGln 152

QY 242 AGGACCTTTGCCAATAGCACTGGAAGCCCAAGAAATGTCCTCAGAACGAGATCTTGCCA 301

Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172

QY 302 TCTGACGCTCTGCTTTTTCAGTCGGTGTGCTGATGCTTCCATGATGATCAAGTGT 361

Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrllysCys 192

QY 362 ATGAGGAGGAGGCTCATTTTCCTGCTATGTTCTTTGGGATCTGGGATCCACGCTA 421

Db 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212

QY 422 GCATCTNCTTACTTTGGGAAACCCAGCGCGCGGAAAGCCAAAG 466

Db 213 SerValSerIleLeuLeuTrpAlaThrGlnArgAlaGlyAlaLys 227

RESULT 7

AAU04295

ID AAU04295 standard; protein; 229 AA.

XX AC AAU04295;

XX DT 24-OCT-2001 (first entry)

XX DE Transforming growth factor (TGF) alpha HIII.

XX KW Human, TGF alpha HIII; transforming growth factor alpha HIII; cancer;

XX KW diagnostic; therapeutic; immune disorder; multiple sclerosis;

XX KW systemic lupus erythematosus; human immuno-deficiency virus; HIV;

XX KW hyperproliferative disorder; Gaucher's disease; cardiovascular disease;

XX KW Scimitar syndrome; Chaga's cardiomyopathy; coronary arteriosclerosis;

XX KW angiogenic disorder; corneal graft; neovascularisation; wound healing;

XX KW diabetic retinopathy; neurological disorder; Huntington's chorea;

XX KW Alzheimer's disease; Parkinson's disease.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..25

XX FT Protein 26..229

XX FT /label= Signal\_peptide

XX FT /note= "Mature TGF alpha HIII"

XX FT Active-site 126..177

XX FT Region 178..204

XX FT /note= "Transmembrane region"

XX PN WO200140251-A1.

XX PD 07-JUN-2001.

XX PF 01-DEC-2000; 2000WO-US032745.

XX PR 02-DEC-1999; 99US-0168387P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Wei Y;

XX DR WPI; 2001-441480/47.

XX DR N-PSDB; AAS08543.

XX PT Nucleic acid encoding human transforming growth factor alpha III (TGFA),

XX PT useful for preventing, diagnosing and/or treating e.g. Cancer and

XX PT Parkinson's disease.

XX PS Claim 11; Fig 1; 302pp; English.

XX CC The sequence represents the amino acid sequence of human transforming

XX CC growth factor (TGF) alpha HIII. TGF alpha HIII nucleic acid and protein

XX CC may be used in the prevention, diagnosis and treatment of diseases

XX CC associated with inappropriate polypeptide expression, for example immune

XX CC disorders (e.g. multiple sclerosis, systemic lupus erythematosus and

XX CC human immuno-deficiency virus (HIV) infections), hyperproliferative

XX CC disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases

XX CC (e.g. Scimitar syndrome, Chaga's cardiomyopathy and coronary

XX CC arteriosclerosis), angiogenic disorders (e.g. corneal graft

XX CC neovascularisation and diabetic retinopathy), neurological disorders

XX CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease),

XX CC infectious diseases and/or for promoting wound healing, regeneration

XX CC and/or chemotaxis (full details given in specification). Additionally,

XX CC the nucleic acid may be used to produce the secreted polypeptides, by

XX CC inserting the nucleic acids into a host cell and culturing the cell to

XX CC express the protein. It may also be used as a DNA probe in diagnostic

XX CC assays to detect and quantitate the presence of similar nucleic acid

XX CC sequences in samples, and therefore which patients may be in need of

XX CC restorative therapy. The polypeptides may also be used as antigens in the

XX CC production of antibodies against TGF alpha HIII and in assays to identify

XX CC modulators of TGF alpha HIII. The anti-TGF alpha HIII antibodies may also

XX CC be used as diagnostic agents for detecting the presence of TGF alpha HIII

XX CC in samples (e.g. by enzyme linked immunosorbant assay (ELISA))

XX SQ Sequence 229 AA;

Alignment Scores:

Pred. No.:	4.61e-63	Length:	229
Score:	690.00	Matches:	128
Percent Similarity:	89.68%	Conservative:	11
Best Local Similarity:	82.58%	Mismatches:	16
Query Match:	77.70%	Indels:	1
DB:	4	Gaps:	0

US-09-773-476-294 (1-489) x AAU04295 (1-229)

QY 3 CTGAGGCTAGACTTTCAGACTGTTCCCT-GAGGATCTGCTCCAAACTTTTACAGGCT 61

Db	73	LeuGlyLeuAspLeuGlnAsnCySerLeuGluAspProGlyProAsnPheHisGlnAla	92
Qy	62	TATACTGCTATTATCATAGACCTTCAGGCAAAATCCTCTCAAGGATGATTGGCCCAACACC	121
Db	93	HisThrThrValIleileAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr	112
Qy	122	TTCCGTGGGTTTACTCAGCTGAGACTCTGATCTACTACCAAGATGTTCCCTGTCCTGGA	181
Db	113	PheArgGlyPheThrGlnLeuGlnThrLeuIleLeuProGlnH.sValAsnCysProGly	132
Qy	182	GGTAGTAATGCTGGGCAAAATGTTACTTCTTTCAGGACAGCAGATTGCAAGGGCAA	241
Db	133	GlyIleAsnAlaTyrAsnThrIleThrSerTyrIleAspAsnGlnIleCysGlnGlyGln	152
Qy	242	ACGGACCTTTGCAATGACCTGAGACCCAGAAATGTTCTGAGAACGGATCTTGCCA	301
Db	153	LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal	172
Qy	302	TCTGACGGTCCGCTTTTTCAGTGGCTTCTGCTGATGGTTTCCATGGATACAAAGTGT	361
Db	173	ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys	192
Qy	362	ATGAGCGAGGCTCATTTTCACTGCTTATGTTCTTGGGATCTGGGATCCACCAAGCTTA	421
Db	193	MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu	212
Qy	422	GCCATCTCATCTACTTTGGGACCCAGCCGCGGAAAGCAAAG	466
Db	213	SerValSerIleLeuLeuThrAlaThrGlnArgGlyAlaLys	227
RESULT 8			
AAB20112			
ID	AAB20112 standard; protein; 229 AA.		
XX			
AC	AAB20112;		
XX			
DT	30-APR-2001 (first entry)		
XX			
DE	Human immunostimulant PRO240.		
XX			
KW	PRO240: UNQ214; human; immune disease; autoimmune disease; antirheumatic; antiarthritic; antiinflammatory; antianaemic; immunosuppressive;		
KW	antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide;		
KW	dermatological; antipsoriatic; antiasthmatic; antiallergic;		
KW	immunostimulant; serrate; lung cancer.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1..30	/label= Signal_peptide
FT	Modified-site	7..13	/note= "N-myristoylation site"
FT	Modified-site	24..30	/note= "N-myristoylation site"
FT	Protein	31..229	/label= Mature_protein
FT	Modified-site	40..46	/note= "N-myristoylation site"
FT	Modified-site	44..48	/note= "Asn is N-glycosylated"
FT	Modified-site	70..76	/note= "N-myristoylation site"
FT	Modified-site	79..83	/note= "Asn is N-glycosylated"
FT	Modified-site	132..138	/note= "N-myristoylation site"
FT	Modified-site	157..161	/note= "Asn is N-glycosylated"
FT	Modified-site	168..172	/note= "Asn is N-glycosylated"
FT	Modified-site	177..183	/note= "Asn is N-glycosylated"

FT	Region	/note= "N-myristoylation site"
FT		181..193
FT	Domain	/note= "epidermal growth factor domain cysteine pattern signature"
FT		198..213
FT	Modified-site	/note= "transmembrane domain"
FT		205..211
FT		/note= "N-myristoylation site"
XX	MO200105972-A1.	
XX	25-JAN-2001.	
XX	15-MAR-2000; 2000WO-US006884.	
XX	20-JUL-1999; 99US-0144758P.	
XX	(GETH ) GENENTECH INC.	
PI	Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ;	
PI	Gurney AL, Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D;	
PI	Watanabe CK, Wood WI;	
XX	WPI; 2001-103149/11.	
DR	N-PSDB; AAF30054.	
XX	New PRO polypeptides, nucleic acids and (ant)agonists, useful for diagnosing and treating immune-related disorders, such as multiple sclerosis, rheumatoid arthritis and diabetes.	
XX	Claim 20; Fig 10; 127pp; English.	
CC	The present sequence is that of novel human immunomodulator PRO240 (UNQ214), as deduced from cDNA (see AAF30054) isolated from a foetal liver library. PRO240 (25 kDa, pI 7.83) shows sequence homology to chicken C-serrate-1 and Drosophila serrate precursor protein. Expression was observed in lung cancer, 8 squamous carcinomas and in 6/8 adenocarcinomas, in situ and infiltrating components. The invention provides polynucleotides (see AAF30050-62) encoding novel human PRO proteins (see AAB20108-20) including PRO240. Claimed compositions comprising these proteins or their agonists are useful for increasing infiltration of inflammatory cells into a tissue of a mammal, stimulating or enhancing an immune response, or increasing the proliferation of T-lymphocytes in a mammal in response to an antigen. Claimed compositions comprising a PRO polypeptide or its antagonist have the opposite effect. A claimed method for treating an immune related disorder, such as a T cell disorder, involves administering a PRO polypeptide, an agonist antibody or an antagonist antibody. The disorder is selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathy, systemic sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinated diseases (such as multiple sclerosis), autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis and Crohn's disease), gluten-sensitive enteropathy, Whipple's disease, (auto)immune-mediated skin diseases (such as bullous skin disease, erythema multiforme and psoriasis), allergic diseases (such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria), immunologic diseases of the lung and transplantation associated diseases (such as graft rejection and graft-versus-host disease) (all claimed). Claimed methods of diagnosing these disorders comprise detecting the level of expression of the PRO gene. Also claimed are a method of identifying a compound capable of inhibiting the expression or activity of the PRO polypeptide, vectors, host cells, antibodies, and a method of stimulating an immune response in a mammal using PRO240	
XX	Sequence 229 AA;	
SQ	Alignment Scores:	
XX	Pred. No.:	4.61e-63 Length: 229

Score: 690.00 Matches: 128  
 Percent Similarity: 89.68% Conservative: 11  
 Best Local Similarity: 82.58% Mismatches: 16  
 Query Match: 77.70% Indels: 1  
 DB: 4 Gaps: 0

US-09-773-476-294 (1-489) x AAB20112 (1-229)

QY 3 CTGAGGCTAGATCTTCAGACTGCTCCCT-GAGGATCCTGGTCCAAACTTTTACAGGCT 61  
 DB 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92  
 QY 62 TATACCTGCTATTATCATAGACCTTCAGCAATCCCTCAAGGATGATTGGCCACACC 121  
 DB 93 HisThrThrValIleIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112  
 QY 122 TTCGCTGGGTTTACTCAGCTGCAGACTCTCATATCTACCAAGATGTTCCCTGCTCTGGA 181  
 DB 113 PheArgGlyPheThrGlnLeuGlnThrLeuLeuLeuProGlnHisValAsnCysProGly 132  
 QY 182 GGTAGTAATGCTGGGCAATGTTACTTCTTCAAGGACAGCAGATTTCCCAAGGCCAA 241  
 DB 133 GlyIleAsnAlaTrpAsnThrIleThrSerTyIleAspAsnGlnIleCysGlnGlyGln 152  
 QY 242 AGGACCTTTGCAATAGACTGGAAGCCAGAAATGTCTCAGAACGATCTTCTGCA 301  
 DB 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172  
 QY 302 TCTGACGCTCCTGCTCTTTGCGAGTGTGCTGATGCTGATGCTTCCATGATACAAAGTGT 361  
 DB 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyIysCys 192  
 QY 362 ATGAGGACGAGGCTCATTTTCACTGCTTATGCTTCTTTGGGATCTGGATCCACCGCTA 421  
 DB 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212  
 QY 422 GCCATCTNCATTTACTTTTGGGAACCCAGCGCCGGAAGCCAAAG 466  
 DB 213 SerValSerIleLeuLeuTrpAlaThrGlnArgAlaLys 227

# RESULT 9

ID AAB68595 standard; protein; 229 AA.

AC AAB68595;

DT 27-APR-2001 (first entry)

DE PRO240.

XX Cytostatic; PRO protein; tumour; cancer.

XX Homo sapiens.

OS W0200105836-A1.

PN 25-JAN-2001.

XX 20-DEC-1999; 99WO-US030999.

XX 20-JUL-1999; 99US-0144758P.

XX 26-JUL-1999; 99US-0145698P.

XX 08-SEP-1999; 99WO-US020594.

XX 13-SEP-1999; 99WO-US020944.

XX 15-SEP-1999; 99WO-US021090.

XX 05-OCT-1999; 99WO-US023089.

XX 29-NOV-1999; 99WO-US028214.

XX 30-NOV-1999; 99WO-US028313.

XX 02-DEC-1999; 99WO-US028564.

XX (GETH ) GENENTECH INC.

PA Botstein D, Goddard A, Gurney AL, Hillan KJ, Roy NA, Wood WJ;

XX PI

XX WPI; 2001-091968/10.  
 DR N-PSDB; AAF60356.

XX New antibody that binds to a PRO polypeptide, e.g. PRO187 and PRO533,  
 PT useful for diagnosing and treating cancers.

XX Claim 61; Fig 8; 196pp; English.

XX The present invention relates to PRO proteins and coding sequences. The  
 CC present sequence is one such PRO protein. It was found that the PRO genes  
 CC are amplified in the genome of tumour cells. The gene amplification is  
 CC expected to be associated with the overexpression of the gene product and  
 CC contributes to tumorigenesis. Therefore, antagonists of PRO proteins are  
 CC useful for the treatment of benign or malignant tumours, leukaemias,  
 CC lymphoid malignancies and other disorders such as neuronal, glial,  
 CC astrocytal, hypothalamic, glandular, epithelial, inflammatory and  
 CC immunologic disorders

XX Sequence 229 AA;

## Alignment Scores:

Pred. No.: 4.61e-63 Length: 229  
 Score: 690.00 Matches: 128  
 Percent Similarity: 89.68% Conservative: 11  
 Best Local Similarity: 82.58% Mismatches: 16  
 Query Match: 77.70% Indels: 1  
 DB: 4 Gaps: 0

US-09-773-476-294 (1-489) x AAB68595 (1-229)

QY 3 CTGAGGCTAGATCTTCAGACTGTTCCCT-GAGGATCCTGGTCCAAACTTTTACAGGCT 61  
 DB 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92  
 QY 62 TATACCTGCTATTATCATAGACCTTCAGCAATCCCTCAAGGATGATTGGCCACACC 121  
 DB 93 HisThrThrValIleIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112  
 QY 122 TTCGCTGGGTTTACTCAGCTGCAGACTCTCATATCTACCAAGATGTTCCCTGCTCTGGA 181  
 DB 113 PheArgGlyPheThrGlnLeuGlnThrLeuLeuLeuProGlnHisValAsnCysProGly 132  
 QY 182 GGTAGTAATGCTGGGCAATGTTACTTCTTCAAGGACAGCAGATTTCCCAAGGCCAA 241  
 DB 133 GlyIleAsnAlaTrpAsnThrIleThrSerTyIleAspAsnGlnIleCysGlnGlyGln 152  
 QY 242 AGGACCTTTGCAATAGACTGGAAGCCAGAAATGTCTCAGAACGATCTTCTGCA 301  
 DB 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172  
 QY 302 TCTGACGCTCCTGCTCTTTGCGAGTGTGCTGATGCTGATGCTTCCATGATACAAAGTGT 361  
 DB 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyIysCys 192  
 QY 362 ATGAGGACGAGGCTCATTTTCACTGCTTATGCTTCTTTGGGATCTGGATCCACCGCTA 421  
 DB 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212  
 QY 422 GCCATCTNCATTTACTTTTGGGAACCCAGCGCCGGAAGCCAAAG 466  
 DB 213 SerValSerIleLeuLeuTrpAlaThrGlnArgAlaLys 227

## RESULT 10

ID AAM51083

XX AAM51083 standard; protein; 229 AA.

XX AC AAM51083;

XX DT 06-JUN-2002 (first entry)

XX Human transforming growth factor alpha H111.

XX

KW Transforming growth factor alpha HIII; TGF alpha HIII; human;  
 KW antiinflammatory; antitumour; vulnery; ophthalmological;  
 KW neuroprotective; antipsoriatic; therapy; diagnosis.

OS Homo sapiens.

FF Key Location/Qualifiers  
 FT Peptide 1..25  
 FT /label= Signal\_peptide  
 FT Protein 26..229  
 FT /label= Mature\_protein  
 FT Active-site 126..177  
 FT Domain 178..204  
 FT /label= Transmembrane\_domain

XX US2002025553-A1.

XX 28-FEB-2002.

XX 01-DEC-2000; 2000US-00726348.

XX 04-JAN-1996; 96US-0011136P.

PR 03-JAN-1997; 97US-00778545.

PR 02-DEC-1999; 99US-0168387P.

XX (WEIY/) WEI Y.

XX Wei Y;

XX WPI; 2002-280092/32.

DR N-PSDB; ABA92166.

XX Isolated nucleic acid molecule encoding Transforming Growth Factor alpha  
 PT HIII is used in preventing, treating or ameliorating a medical condition  
 PT e.g. cardiovascular or autoimmune diseases.

XX Claim 11; Fig 1A-B; 118pp; English.

XX The present sequence is that of human transforming growth factor alpha  
 CC HIII (TGF alpha HIII), a novel member of the TGF family. The amino acid  
 CC sequence was deduced from a cDNA clone (see ABA92166) discovered in a  
 CC human testis cDNA library. The invention provides TGF alpha HIII nucleic  
 CC acid molecules and polypeptides (including the mature protein, full-  
 CC length secreted protein, variants and homologues), vectors, host cells,  
 CC antibodies and recombinant methods for producing the polypeptides. The  
 CC TGF alpha HIII polypeptides and polynucleotides can be used in diagnostic  
 CC methods for detecting disorders related to TGF alpha HIII, and also for  
 CC therapeutic purposes, e.g. to stimulate wound healing to restore normal  
 CC neurological functioning after trauma or AIDS dementia, to treat ocular  
 CC disorders, to target certain cells, to treat kidney and liver disorders,  
 CC to promote hair follicular development, to stimulate angiogenesis for the  
 CC treatment of burns, ulcers and corneal incisions, and to stimulate  
 CC embryogenesis. Autoimmune diseases, disorders of haematopoietic cells,  
 CC allergic reactions, cardiovascular diseases, organ rejection,  
 CC inflammation, and hyperproliferative disorders may also be treated.  
 CC Methods are also provided for identifying agonists and antagonists of TGF  
 CC alpha HIII. Antagonists may be used to inhibit the action of TGF alpha  
 CC HIII polypeptides in the treatment of corneal inflammation, neoplasia  
 CC such as tumours and cancers, and psoriasis

XX Sequence 229 AA;

Alignment Scores:  
 Pred. No.: 4,61e-63 Length: 229  
 Score: 690.00 Matches: 128  
 Percent Similarity: 89.68% Conservative: 11  
 Best Local Similarity: 82.58% Mismatches: 16  
 Query Match: 77.70% Indels: 1  
 DB: 5 Gaps: 0

US-09-773-476-294 (1-489) x AAM51083 (1-229)

QY 3 CTGAGCTAGATCTTCAGAACTGTTCCCT-GAGGATCCGTCGCAACTTTTACAGGCT 61

Db 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92  
 QY 62 TATACTCTATTATCATAGACCTTCAGGCAATCCTCTCAAGGATGATTGGCCAAACACC 121  
 Db 93 HisThrThrValIleIleAspLeuGlnAlaAsnProLeuGlyGlyAspLeuAlaAsnThr 112  
 QY 122 TTCGTGGTTTACTCAGCTGCAGACTCTGATCTACTACCAAGATGTTCCCTCTCTGGA 181  
 Db 113 PheArgGlyPheThrGlnLeuGlnThrLeuIleLeuProGlnHisValAsnCysProGly 132  
 QY 182 GGTAGTAATGCCTGGGACAATGTACTCTTTCAGGACAAGCAGATTTGCCAGGGCAA 241  
 Db 133 GlyIleAsnAlaIleAsnThrIleThrSerIleAspAsnGlnIleCysGlnGlyGln 152  
 QY 242 AGGACCTTTTGCATAGCACTGGAAGCCCAAGAAATGTCTCTGAGACGGATCTTGTGCA 301  
 Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172  
 QY 302 TCTGACGTCCTGGTCTTTTTCAGTGCGTTTGTGCTGATGTTTCCATGATACAGTGT 361  
 Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys 192  
 QY 362 ATGAGGCAGGCTCATTTTCACTGCTTATGTTCTTTGGGATTTGGGATCCACACGCTA 421  
 Db 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212  
 QY 422 GCCATCTNCACTTCTACTTTGGGAAACCCAGCGCGGAAAGCCCAAG 466  
 Db 213 SerValSerIleLeuLeuTPalatThrGlnArgArgLysAlaLys 227

RESULT 11

ABG34033  
 ID ABG34033 standard; protein; 229 AA.

AC ABG34033;

DT 15-JUL-2002 (first entry)

XX Human Pro peptide #4.

XX Human; PRO; secreted protein; transmembrane protein; genetic disorder;  
 KW tumour; cancer.

OS Homo sapiens.

XX WO200224888-A2.

XX 28-MAR-2002.

XX 29-AUG-2001; 2001WO-US027099.

XX 01-SEP-2000; 2000US-0229896P.

XX 05-SEP-2000; 2000US-0230621P.

PR 22-SEP-2000; 2000US-0235147P.

PR 10-NOV-2000; 2000WO-US030873.

PR 12-JAN-2001; 2001US-0261878P.

PR 16-JAN-2001; 2001US-0261910P.

PR 16-JAN-2001; 2001US-0261939P.

PR 25-JAN-2001; 2001US-0264395P.

PR 02-FEB-2001; 2001US-0266421P.

PR 09-FEB-2001; 2001US-0267623P.

PR 28-FEB-2001; 2001WO-US006520.

PR 03-MAR-2001; 2001US-0274399P.

PR 09-APR-2001; 2001US-0280982P.

PR 04-APR-2001; 2001US-0282125P.

PR 04-APR-2001; 2001US-0282199P.

PR 25-MAY-2001; 2001US-0290589P.

PR 01-JUN-2001; 2001WO-US017092.

PR 20-JUN-2001; 2001WO-US019692.

PR 29-JUN-2001; 2001WO-US021066.

PR 09-JUL-2001; 2001WO-US021735.  
PA (GETH) GENENTECH INC.  
XX Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC;  
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S;  
XX WPI; 2002-362426/39.  
DR N-PSDB; ABK69964.  
XX New PRO polypeptides and polynucleotides encoding the polypeptides,  
PT useful in gene therapy, chromosome identification, tissue typing, or for  
PT genetic analysis of individuals with genetic disorders.  
XX Claim 11; Fig 8; 218pp; English.  
XX This invention relates to the cDNA and protein sequences of novel  
CC secreted and transmembrane polypeptides PRO polypeptides. The invention  
CC also comprises a method for producing the proteins of the invention by  
CC recombinant means and antibodies specific for the protein of the  
CC invention. The antibody may be used for detecting the PRO proteins of the  
CC invention and may be used to modify their activity. Polynucleotides may  
CC be used as hybridisation probes for a cDNA library to isolate the full-  
CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation  
CC probes for mapping the gene which encodes that PRO and for genetic  
CC analysis of individuals with genetic disorders, in assays to identify  
CC other proteins or molecules involved in binding reaction, to generate  
CC transgenic animals or knock-out animals which in turn are useful in the  
CC development and screening of therapeutically useful reagents, for  
CC chromosome identification, and tissue typing. The PRO polypeptides are  
CC useful in gene therapy, and as molecular weight markers for protein  
CC electrophoresis purposes. The sequences may also be used to detect  
CC overexpression on PRO polypeptides in cancerous tumours and for screening  
CC for differentially expressed genes using microarray technology. The  
CC present sequence represents a human PRO protein of the invention  
XX SQ Sequence 229 AA;  
Alignment Scores:  
Pred. No.: 4,61e-63 Length: 229  
Score: 690.00 Matches: 128  
Percent Similarity: 89.68% Conservative: 11  
Best Local Similarity: 82.58% Mismatches: 16  
Query Match: 77.70% Indels: 1  
DB: 5 Gaps: 0  
US-09-773-476-294 (1-489) x ABG34033 (1-229)  
Qy 3 CTGAGGCTAGATCTTACAGACTGTCCTC-CAGATCCTGCTGCAACTTTTACAGGCT 61  
Db 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnHeHisGlnAla 92  
Qy 62 TAACTGCTATTATCATAGACCTTCAGGCAATCCTCTCAAGGATGATTTGGCCACAC 121  
Db 93 HisThrThrValIleIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112  
Qy 122 TTCGCTGGTGTACTAGCTGCAGACTCTGATCTACTACCAAGATGTCCTGCTCTGGA 181  
Db 113 PheArgGlyPheThrGlnLeuGlnThrLeuLeuLeuProGlnHisValAsnCysProGly 132  
Qy 182 GGATAGTAACTGCTGGGCAATGTTACTCTTCTTCAAGGACAGCAGATTTGCCAAGGCCAA 241  
Db 133 GlyIleAsnAlaTrpAsnThrIleThrSerTyIleAspAsnGlnIleCysGlnGlyGln 152  
Qy 242 AGGACCTTTCATACATGAGCCAGCCAGAAATGTGCTCCTGAGAACGGATCTTGTGCA 301  
Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172  
Qy 302 TCTGACGCTCCTGCTCTTTTGCAGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361  
Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyTyLysCys 192

Qy 362 ATGAGGACAGGCTCATTTTCTTATGTTCTTTGGATTCCTGGATCCACCAAGCTA 421  
Db 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrieu 212  
Qy 422 GCCATCTTCATCTTCTTGGGAACCCAGCGCCGGAAGCAAG 466  
Db 213 SerValSerIleLeuLeuTrpAlaThrGlnArgArgLysAlaLys 227  
RESULT 12  
ABU71417  
ID ABU71417 standard; protein; 229 AA.  
XX AC ABU71417;  
XX DT 09-JUN-2003 (first entry)  
XX DE Human neoplasia inhibiting PRO polypeptide PRO240.  
XX Human; tumour; cancer; neoplasia; liver cancer; sarcoma; breast cancer;  
KW ovarian cancer; renal cancer; colorectal cancer; melanoma;  
KW uterine cancer; prostate cancer; lung cancer; bladder cancer; leukaemia;  
KW gastric cancer; pancreatic cancer; vulval cancer; thyroid cancer;  
KW central nervous system cancer; hepatic carcinoma; glioblastoma;  
KW neuronal disorder; glial disorder; astrocytic disorder;  
KW hypothalamic disorder; glandular disorder; macrophagal disorder;  
KW epithelial disorder; stromal disorder; blastocellic disorder;  
KW inflammatory disorder; angiogenic disorder; immunologic disorder.  
XX OS Homo sapiens.  
XX PN US2002192209-A1.  
XX PD 19-DEC-2002.  
XX PF 30-NOV-2001; 2001US-00001054.  
XX PR 17-SEP-1997; 97US-0059114P.  
PR 27-MAR-1998; 98US-0079689P.  
PR 30-MAR-1998; 98US-0079920P.  
PR 24-APR-1998; 98US-0082999P.  
PR 29-APR-1998; 98US-0083545P.  
PR 12-MAY-1998; 98US-0085149P.  
PR 02-JUN-1998; 98US-0087607P.  
PR 11-JUN-1998; 98US-0088589P.  
PR 25-JUN-1998; 98US-0090691P.  
PR 17-AUG-1998; 98US-0096891P.  
PR 10-SEP-1998; 98US-0099803P.  
PR 14-SEP-1998; 98US-0100263P.  
PR 15-SEP-1998; 98US-0100390P.  
PR 23-SEP-1998; 98US-0101476P.  
PR 10-NOV-1998; 98US-0107783P.  
PR 18-NOV-1998; 98US-010849P.  
PR 19-NOV-1998; 98US-00180997.  
PR 15-DEC-1998; 98US-0112420P.  
PR 22-DEC-1998; 98US-00218517.  
PR 22-DEC-1998; 98US-0113296P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 12-JAN-1999; 99US-0115554P.  
PR 12-JAN-1999; 99US-0115558P.  
PR 20-JAN-1999; 99US-0116533P.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99US-0123618P.  
PR 12-APR-1999; 99US-00284291.  
PR 20-APR-1999; 99WO-US008615.  
PR 27-APR-1999; 99US-0131294P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 22-JUN-1999; 99US-0140650P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 25-AUG-1999; 99US-00380137.  
PR 25-AUG-1999; 99US-00380138.



PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 09-SEP-1999; 99US-00380913.  
PR 18-OCT-1999; 99US-00403297.  
PR 29-OCT-1999; 99US-0162506P.  
PR 10-NOV-1999; 99US-00423741.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 09-DEC-1999; 99US-0170262P.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030939.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US0003565.  
PR 18-FEB-2000; 2000WO-US0004341.  
PR 18-FEB-2000; 2000WO-US0004342.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 03-MAR-2000; 2000US-0187202P.  
PR 15-MAR-2000; 2000WO-US006984.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 08-NOV-2000; 2000US-00709238.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872034.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 14-JUN-2001; 2001US-00882636.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 30-JUL-2001; 2001US-00918585.  
PR 06-AUG-2001; 2001US-00924419.  
PR 09-AUG-2001; 2001US-00927796.  
PR 13-AUG-2001; 2001US-00929404.  
PR 28-AUG-2001; 2001US-00941992.  
PR 29-AUG-2001; 2001WO-US027099.  
PR 04-SEP-2001; 2001US-00946374.  
PA (GETH ) GENENTECH INC.  
XX Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;  
PI Shelton DL, Smith V, Watanabe CK, Wood WI;  
XX N-P6DB; ACA57990.  
DR WPI; 2003-328851/06.  
DR N-P6DB; ACA57990.  
XX Novel isolated PRO polypeptides e.g. PRO240, PRO381, PRO540, useful for  
PT treating tumor, preferably cancer, or for treating neuronal, glial,  
PT hypothalamic, stromal, inflammatory, angiogenic and immunologic  
PT disorders.  
XX Claim 32; Fig 2; 186pp; English.  
PS The invention relates to an isolated secreted and transmembrane  
XX polypeptide, designated as PRO polypeptide, PRO polypeptide lacking its  
CC associated signal peptide or PRO polypeptide extracellular domain with or  
CC without its associated signal peptide. The PRO polypeptide or an antibody  
CC binding to it is useful for inhibiting the growth of a tumor cell. A  
CC composition containing a PRO polypeptide is useful for inhibiting  
CC neoplastic cell growth or for treating a tumor, preferably cancer (such  
CC as liver, breast, ovarian, renal, colorectal, uterine, prostate, lung,  
CC bladder, gastric, pancreatic, vulval, thyroid, central nervous system

CC cancer, hepatic carcinomas, sarcomas, glioblastomas, melanoma or  
CC leukemia) in a mammal. The PRO polypeptide is useful for identifying its  
CC agonists. The PRO polypeptide or an antibody binding to it is useful in  
CC the preparation of a medicament for treating a condition which is  
CC responsive to the PRO polypeptide or an antibody binding to it. The PRO  
CC polypeptide or an antibody binding to it is also useful for treating  
CC neuronal, glial, astrocytic, hypothalamic, glandular, macrophageal,  
CC epithelial, stromal, blastocoeic, inflammatory, angiogenic and  
CC immunologic disorders. The present sequence represents the amino acid  
CC sequence of a PRO polypeptide of the invention  
XX  
SQ Sequence 229 AA;  
Alignment Scores: 4.61e-63 Length: 229  
Pred. No.: 690.00 Matches: 128  
Percent Similarity: 89.68% Conservative: 11  
Best Local Similarity: 82.58% Mismatches: 16  
Query Match: 77.70% Indels: 1  
DB: 6 Gaps: 0  
US-09-773-476-294 (1-489) x ABU71417 (1-229)  
QY 3 CTGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCCTGGTCCAACTTTTACAGGCT 61  
DB 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92  
QY 62 TATAGCTATTATCATAGACCTTCAGGCAATCTCTCAAGGATGATTGGCCACACC 121  
DB 93 HisThrThrValIleIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112  
QY 122 TTCGCTGGTTTACTCAGCTGCAGACTCTGATATCTACCACAGATGTTCCCTGCTCTGGA 181  
DB 113 PheArgGlyPheThrGlnLeuGlnThrLeuLleLeuProGlnHisValAsnCysProGly 132  
QY 182 GGTAGTAATCCCTGGGCAATGTTACTTCTTCAAGGACAAGCAGATTTCCTCAAGGGCAA 241  
DB 133 GlyIleAsnAlaTrpAsnThrIleThrSerTyrIleAspAsnGlnIleCysGlnGlyGln 152  
QY 242 AGGACCTTTGCCAATAGCACTGGAGCCAGAAATGTTCTCTGAGACGATCTTGTGCA 301  
DB 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172  
QY 302 TCTGACGCTCTCGTCTTTTGCAGTGGTGTGTGCTGATGTTTCCATGATGATCAAGTGT 361  
DB 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys 192  
QY 362 ATGAGGAGGGCTCATTTTCACTGCTTATGTTCTTTGGGATTTCTGGATCCACACGCTA 421  
DB 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212  
QY 422 GCCATCTNCATTCTTCTTGGGAACCCAGCGCCGGAAGCCCAAG 466  
DB 213 SerValSerIleLeuLeuTrpAlaThrGlnArgArgLysAlaLys 227  
RESULT 13  
ADA01276  
ID ADA01276 standard; protein; 229 AA.  
XX  
AC ADA01276;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
DE Human PRO polypeptide #4.  
XX  
KW Human; PRO; secreted polypeptide; transmembrane polypeptide;  
KW tumor necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;  
KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;  
KW microvascular endothelial cell; endothelial cell tube formation;  
KW sports-related joint problem; articular cartilage defect; osteoarthritis;  
KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.  
OS Homo sapiens.

XX US2003068779-A1.  
 XX 10-APR-2003.  
 XX 16-SEP-2002; 2002US-00245107.  
 XX 09-MAY-2001; 2001US-0290589P.  
 XX 29-AUG-2001; 2001WO-US027099.  
 XX 18-JUL-2002; 2002US-00197942.  
 XX (GETH ) GENENTECH INC.  
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
 XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
 XX Fong S;  
 XX WPI; 2003-625484/59.  
 XX N-PSDB; ADA01275.  
 XX Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for  
 XX stimulating proliferation of human microvascular endothelial cells, and  
 XX PRO6018 polypeptide useful for stimulating proliferation of chondrocyte  
 XX cells.  
 XX Claim 11; Fig 8; 307pp; English.  
 XX The invention relates to isolated human PRO polypeptides (secreted and  
 XX transmembrane polypeptides) and the polynucleotides encoding them. The  
 XX invention also relates to an antibody which specifically binds to a PRO  
 XX polypeptide, a method for stimulating the release of tumour necrosis  
 XX factor-alpha (TNF-alpha) from human blood, a method for stimulating the  
 XX proliferation or differentiation of chondrocyte cells and a method for  
 XX detecting the presence of a tumour in a mammal (e.g. adrenal, lung,  
 XX colon, breast, prostate, rectal, cervical and liver tumours). The  
 XX polynucleotides are useful in molecular biology, including uses as  
 XX hybridisation probes, in chromosome and gene mapping, in generating  
 XX antisense RNA and DNA and in gene therapy. The polynucleotides may also  
 XX be used in preparing PRO polypeptides by recombinant techniques and in  
 XX generating either transgenic animals or knock-out animals which are  
 XX useful in the development and screening of therapeutically useful  
 XX reagents. The PRO polypeptides or antibodies are used in preparing a  
 XX medicament for treating a condition responsive to the polypeptides or  
 XX antibodies, such as tumours, for stimulating and inhibiting proliferation  
 XX of human microvascular endothelial cells, for inducing endothelial cell  
 XX tube formation and for treating sports-related joint problems, articular  
 XX cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence  
 XX represents a human PRO polypeptide of the invention.  
 XX  
 SQ Sequence 229 AA;  
 Alignment Scores:  
 Pred. No.: 4.61e-63 Length: 229  
 Score: 690.00 Matches: 128  
 Percent Similarity: 89.68% Conservative: 11  
 Best Local Similarity: 82.58% Mismatches: 16  
 Query Match: 77.70% Indels: 1  
 DB: 6 Gaps: 0  
 US-09-773-476-294 (1-489) x ADA01276 (1-229)  
 QY 3 CTGAGGCTAGACTCTCAGAACTGTCCT- GAGGATCTGGTCCAACTTTTACAGGCT 61  
 Db 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPhenHisGlnAla 92  
 QY 62 TATACGTCTATTATCATAGACTTCAGGAAATCTCTCAAGATGATTTGGCCAAACACC 121  
 Db 93 HisThrThrValIleLeuAspLeuGlnAlaAsnProLeuLysLeuAspLeuAlaAsnThr 112  
 QY 122 TTCGGTGGGTTTACTCAGCTGCAGACTCTGATACCTACCAAGATGTTCCCTGCTCTGGA 181  
 Db 113 PheArgGlyPheThrGlnLeuGlnThrLeuIleLeuProGlnHisValAsnCysProGly 132

QY 182 GGTAGTAATGCTGGGCAATGTTACTTCTTCAAGGACAGCAGATTGCCAAGGGCAA 241  
 Db 133 GlyIleAsnAlaIleAsnThrIleThrSerTyrIleAspAsnGlnIleCysGlnGlyGln 152  
 QY 242 AGGACACCTTTGCAATAGCAGCTCGGAAGCCAGAAATGCTCTGAGAACCGGATCTGTGCA 301  
 Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172  
 QY 302 TCTGACGCTCTGGTCTTTTTCAGTGGCTTGTGCTGCTGATGGTTTCCATGGATACAAAGTGT 361  
 Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys 192  
 QY 362 ATGAGGACAGGCTCATTTTTCATCTGCTTATGTTCTTGGGATTTCTGGATCCACCAAGCTA 421  
 Db 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrIleu 212  
 QY 422 GCCATCTTNCATTTCTACTTTGGGAAACCCAGCGCCGGAAGCCAAAG 466  
 Db 213 SerValSerIleLeuLeuTrpAlaThrGlnArgArgLysAlaLys 227  
 RESULT 14  
 ADA43705  
 ID ADA43705 standard; protein; 229 AA.  
 XX AC ADA43705;  
 XX DT 20-NOV-2003 (first entry)  
 XX DE Human secreted/transmembrane polypeptide PRO240.  
 XX Human; PRO; secreted protein; transmembrane protein;  
 XX endothelial cell tube formation; chondrocyte cell differentiation;  
 XX microvascular endothelial cell; tumour; lung tumour; colon tumour;  
 XX breast tumour; prostate tumour; rectal tumour; kidney tumour;  
 XX liver tumour; cytostatic; vaccine.  
 XX Homo sapiens.  
 OS US2003064474-A1.  
 PN 03-APR-2003.  
 PD 16-SEP-2002; 2002US-00245859.  
 XX 29-AUG-2001; 2001WO-US027099.  
 PR 18-JUL-2002; 2002US-00197942.  
 XX (GETH ) GENENTECH INC.  
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
 XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;  
 XX Fong S;  
 XX WPI; 2003-605867/57.  
 DR N-PSDB; ADA43704.  
 XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or  
 XX PRO21383, useful in molecular biology, chromosome and gene mapping, in  
 XX generating antisense RNA and DNA, and in gene therapy.  
 XX Claim 11; Fig 8; 308pp; English.  
 XX The invention relates to an isolated secreted/transmembrane (PRO)  
 XX polypeptide, having at least 80% sequence identity to a sequence selected  
 XX from any one of the 57 amino acid sequences given in specification, or to  
 XX a sequence encoded by a nucleic acid molecule selected from any one of  
 XX the nucleic acids deposited under any of the ATCC accession numbers given  
 XX in specification, or a sequence having at least 80% identity to PRO  
 XX lacking its associated signal peptide, an extracellular domain of PRO  
 XX with or without its associated signal peptide. Also included are vectors,  
 XX transformed host cells, anti-PRO antibodies, the nucleic acids encoding  
 XX PRO, PRO fusion proteins, inducing endothelial cell tube formation (by  
 XX administering PRO281, PRO1560, PRO189, PRO4499, PRO6000,

QY	3	CTGAGGCTAGATCTTCAGAACTGTGTCCTCTCAGATCCTCGTCCCAACTTTTTACAGGCT	61
Db	73	LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla	92
QY	62	TATACTGCTATTATCATAGACTTCAGGCAAACTCCTCTCAAGGATGATTGGCCAAACCC	121
Db	93	HisThrThrValIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr	112
QY	122	TTCCGTGGGTTTACTCAGCTCGAGACTCTGATCTACTACACAAAGATGTTCCCTGTCCTGGA	181
Db	113	PheArgGlyPheThrGlnLeuGlnThrLeuLeuLeuProGlnHisValAsnCysProGly	132
QY	182	GGTAGTAATGCTCGGACCAATGTTACTTCTTCAAGGACAAAGCAGAGATTGGCCAAAGGCCAA	241
Db	133	GlyIleAsnAlaTrpAsnThrIleThrSerTyrIleAspAsnGlnIleCysGlnGlyGln	152
QY	242	AGGGACCTTTGCAATAGCACTCGAAGCCAGAAATGTCTCTCAGAACCGATCTGTGCA	301
Db	153	LysAsnLeuCysAsnAsnThrGlyAspProGlnMetCysProGluAsnGlySerCysVal	172
QY	302	TTTGACGGTCTCGTCTTTTGACGTGGTTTGCTGCTCATGTTTCATGATCAGATCAGTGT	361
Db	173	ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys	192
QY	362	ATGAGGACGGGCTCATTTTCACTGCTATGTTCTTTGGGATCTGGGATCCACACGCTTA	421
Db	193	MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyLeuGlyAlaThrThrLeu	212
QY	422	GCATCTCNCAATTCTATTGTGGGGAACCCAGCGCCGGAAAGCCCAAG	466
Db	213	SerValSerIleLeuLeuTrpAlaThrGlnArgArgLysAlaLys	227

ADA43473

XX

1

The invention relates to an isolated secreted/transmembrane (PRO) polypeptide, having at least 80% sequence identity to a sequence selected from any one of the 57 amino acid sequences given in specification, or to a sequence encoded by a nucleic acid molecule selected from any one of the nucleic acids deposited under any of the ATCC accession numbers given in specification, or a sequence having at least 80% identity to PRO lacking its associated signal peptide, an extracellular domain of PRO with or without its associated signal peptide. Also included are vectors, transformed host cells, anti-PRO antibodies, the nucleic acids encoding PRO, PRO fusion proteins, including endothelial cell tube formation (by administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933, or PRO34274 polypeptide or its agonist) and an oligonucleotide probe derived from any one of the above nucleotide sequences. PRO6018 polypeptide is useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080 and PRO21383 polypeptides are useful for stimulating the proliferation of human microvascular endothelial cells, PRO6071, PRO4487 and PRO6006 polypeptides are useful for inhibiting the proliferation of human microvascular endothelial cells. PRO polypeptides are useful for detecting the presence of tumour in a mammal, including tumours of lung, colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO10275, PRO21207, PRO20933 and PRO34274 polypeptides are useful for inducing endothelial cell tube formation. PRO or the antibody are useful in the preparation of a medicament for treating a condition responsive to PRO polypeptide. The oligonucleotide probes are useful for isolating genomic and cDNA nucleotide sequences, for measuring or detecting the expression of an associated gene, and as antisense probes. PRO nucleic acid is useful as a hybridisation probe, in chromosome and gene mapping, in the generation of antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The present sequence represents a PRO protein.

Sequence 229 AA:

Score: 690.00 Matches: 128  
Percent Similarity: 89.68% Conservative: 11  
Best Local Similarity: 82.58% Mismatches: 16  
Query Match: 77.70% Indels: 1  
DB: 6 Gaps: 0

US-09-773-476-294 (1-489) x ADA43473 (1-229)

Qy	3	CTGAGGCTAGACTCTTCAGACTGTTCCCT-GAGGATCCTGGTCCAACTTTTACAGGCT	61
Db	73	LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla	92
Qy	62	TATACTGCTATTATCATAGACCTTCAGGCAATCCTCTCAAGGATGATTTGGCCAAACACC	121
Db	93	HisThrThrValIleIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr	112
Qy	122	TTCGTCGGGTTTACTCAGCTCCAGACTCTCATACTACCAAGATGTTCCCTCTCCTGGA	181
Db	113	PheArgGlyPheThrGlnLeuGlnThrLeuIleLeuProGlnHisValAsnCysProGly	132
Qy	182	GGTAGTAATGCTGGGACAATGTTACTTCTTCAAGGACAAGCAGATTTGCCAAGGGCAA	241
Db	133	GlyIleAsnAlaIleAsnThrIleThrSerTyrIleAspAsnGlnIleCysGlnGlyGln	152
Qy	242	AGGACCTTTTGCAATAGCACTGGAGCCAGAAATGTCTCTGAGAACGGATCTTGTGCA	301
Db	153	LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal	172
Qy	302	TCTGACGGTCTGCTCTTTTCAGTGGGTTGTGCTGATGTTTCCATGGATACAAAGTGT	361
Db	173	ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys	192
Qy	362	ATGAGGCAGGGCTCATTTTCACTGCTTATGTTCTTTGGGATTTCTGGATCCACCGCTA	421
Db	193	MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu	212
Qy	422	GCCATCTNCATTTCTATTGGGGAACCCAGCGCGGAAAGCCAAAG	466
Db	213	SerValSerIleLeuLeuTrpAlaThrGlnArgArgLysAlaLys	227

Search completed: June 25, 2004, 09:13:51  
Job time : 58 secs

OM nucleic - protein search, using frame\_plus\_n2p model  
Run on: June 25, 2004, 09:11:53 ; Search time 17 Seconds  
(without alignments)  
5533.842 Million cell updates/sec

Title: US-09-773-476-294  
Perfect score: 888  
Sequence: 1 gactgagctagattcttcag.....tnatgagccacacaagactt 489

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283366 segs, 96191526 residues  
Total number of hits satisfying chosen parameters: 566732  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ n2p.model -DEV=xlp  
-O=/cpn2\_1/USPTO spoel\_p/US09773476/runat\_25062004\_090847\_5839/app\_query.fasta\_1.647  
-DB=PIR78 -OFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09773476 @CGN 1 1 38 @runat\_25062004\_090847\_5839 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	113	12.7	1203	A49175	Notch B protein -
2	112	12.6	2471	A49128	cell-fate determin
3	103	11.6	2318	S45306	notch 3 protein -
4	103	11.6	2531	A46019	notch-1 protein -
5	102	11.5	2703	A24420	notch protein - fr
6	100.5	11.3	308	JC7125	epidermal growth f
7	100.5	11.3	1722	E89753	protein FilC7.4 (i
8	99	11.1	2809	T30213	G-cadherin - sea u
9	98.5	11.1	1712	A38261	masking protein pr
10	98.5	11.1	2311	S78549	notch3 protein - h
11	98	11.0	2531	S18188	notch protein homo
12	97.5	11.0	1964	T09059	notch4 - mouse
13	95.5	10.8	385	A54785	predipocyte facto
14	95.5	10.8	1394	A35626	transforming growt

15	95	10.7	616	2	T29234	hypothetical prote
16	95	10.7	675	1	KXRTS	plasma protein S p
17	95	10.7	4391	2	A38096	perlecan precursor
18	94.5	10.6	1220	2	A56136	jagged protein pre
19	94.5	10.6	2437	2	S42612	transmembrane prot
20	94	10.6	383	2	S53716	delta-like homeoti
21	94	10.6	2352	2	T30201	Notch homolog prot
22	93.5	10.5	2531	2	T31070	notch homolog - se
23	93.5	10.5	2555	2	A40043	notch protein homo
24	92.5	10.4	2524	2	A35844	notch protein - Af
25	92.5	10.4	2907	2	A57278	fibrillin-2 precu
26	92.5	10.4	2918	2	A54105	fibrillin-2 precu
27	92.5	10.4	4544	1	S02392	alpha-2-macroglobu
28	92	10.4	861	2	A48025	Notch homolog Motc
29	91	10.2	1408	2	S16148	gene serrate prote
30	90.5	10.2	642	2	S53433	plasma protein S p
31	90.5	10.2	4545	1	S25111	alpha-2-macroglobu
32	89.5	10.1	473	2	A56175	adhesive plaque pr
33	89.5	10.1	1820	2	A55494	latent transformin
34	89	10.0	1064	2	A40136	fibropellin Ia - s
35	88.5	10.0	385	2	S53718	homeotic protein d
36	88.5	10.0	685	2	S78040	fibulin, splice fo
37	88.5	10.0	705	2	S34968	fibulin, splice fo
38	88	9.9	2531	2	T16743	hypothetical prote
39	87.5	9.9	1620	2	T27283	hypothetical prote
40	87	9.8	2180	2	T29764	hypothetical prote
41	87	9.8	2871	2	A55567	fibrillin I - bovi
42	87	9.8	2871	2	A55624	fibrillin-1 precu
43	87	9.8	3002	2	A47221	fibrillin 1 precu
44	86	9.7	259	2	T21011	hypothetical prote
45	86	9.7	1469	2	B36665	slit protein 2 pre

ALIGNMENTS

RESULT 1  
A49175  
Notch B protein - mouse (fragment)  
N:Alternate names: Notch homolog  
C:Species: Mus musculus (house mouse)  
C:Date: 21-Jan-1994 #sequence revision 05-Jan-1996 #text\_change 08-Sep-2002  
C:Accession: A49175; PH1570; S32113  
R:Lardelli, M., Lendahl, U.  
Exp. Cell Res. 204, 364-372, 1993  
A:Title: Notch A and Notch B--two mouse Notch homologues coexpressed in a wide variety of  
A:Reference number: A49175; MUID:93178563; PMID:8440332  
A:Accession: A49175  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-1203 <LAR>  
A:Cross-references: EMBL:X68279; NID:g287989; PIDN:CAA48340.1; PID:g287990  
A:Experimental source: embryo  
A:Note: sequence extracted from NCBI backbone (NCBIP:126158)  
C:Comment: This protein has many EGF repeats and lin-12/Notch repeats.  
C:Comment: This protein is one of the neurogenic proteins controlling the decision between  
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology  
F:143-174/Domain: EGF homology <EGX1>  
F:482-513/Domain: EGF homology <EGF1>  
F:560-591/Domain: EGF homology <EGF>  
F:674-705/Domain: EGF homology <EGX2>  
F:712-743/Domain: EGF homology <EGF3>  
F:836-867/Domain: EGF homology <EGX3>

Alignment Scores:  
Pred. No.: 0.00524  
Score: 113.00  
Percent Similarity: 33.58%  
Best Local Similarity: 28.36%  
Query Match: 12.73%  
DB: 2  
Length: 1203  
Matches: 38  
Conservative: 7  
Mismatch: 36  
Indels: 53  
Gaps: 6

US-09-773-476-294 (1-489) x A49175 (1-1203)

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QY 98 CTCAGGATGATTTGGCCACACCTTCCGTGGGTTTACTCAGCTGCAGACTCTGATACTA 157
   :: ||| ||| ||| |||
Db 595 IleAsnAspCysLeuAlaAsn----- 601

QY 158 CCACAAGATGTTCCCTGCTGGAGGTAGTAATCCCTGGGACAAATGTTACTTTTCAAG 217
   ||| ||| ||| ||| ::| ||| ||| |||
Db 602 -----ProCysGlnAsnGlySerCysValAspHisValAsnThrPheSer 617

QY 218 -----GACAAGCAGATTTGCCAAGGGCAAGGGACCTT 250
   ||| ||| ||| ||| ::|
Db 618 CysGlnCysHisProGlyPheIleGlyAspys-----CysGlnThrAspMetAsnGlu 635

QY 251 TGCATAGCACTGGAAGCCAGAAATGTCTCCTGAGAACGGATCTTGTGCATCTGACGGT 310
   ||| ||| ||| ||| ::| ||| ||| |||
Db 636 CysLeuSer-----GluProCysLysAsnGlyGlyThrCys---SerAspTyr 650

QY 311 CCTGGTCTTTTGCAGTGGTTGTGCTGATGTTTCCATGCATACAAAGTGTATGAGGCAG 370
   ||| ||| ||| ||| ||| ||| ||| |||
Db 651 ValAsnSerTyrThrCysThrCysProAlaGlyPheHisGlyValHisCysGluAsnAsn 670

QY 371 -----GGC 373

Db 671 IleAspGluCysThrGluSerSerCysPheAsnGlyGlyThrCysValAspGlyIleAsn 690

QY 374 TCATTTTCACTGCTTATGTTCTTGGGATTTCTGGATCCA 413
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Db 691 SerPheSer-CysLeuCysProValGlyPheThrGlyPro 703

RESULT 2
cell-fate determining gene Notch2 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 02-Aug-2002
C:Accession: A49128
F:Weinmaster, G.; Roberts, V.J.; Lemke, G.
Development 116, 931-941, 1992
A:Title: Notch2: a second mammalian Notch gene.
A:Reference number: A49128; MUID:93202015; PMID:1295745
A:Accession: A49128
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-2471 <WEI>
A:Experimental source: Schwann cell
A>Note: sequence extracted from NCBI backbone (NCBIP:127811)
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:264-295/Domain: EGF homology <EGX1>
F:799-830/Domain: EGF homology <EGF1>
F:877-908/Domain: EGF homology <EGX2>
F:1029-1060/Domain: EGF homology <EGF>
F:1067-1098/Domain: EGF homology <EGX3>
F:1153-1184/Domain: EGF homology <EGF3>
F:1191-1222/Domain: EGF homology <EGX4>
F:1876-1908/Domain: ankyrin repeat homology <AN1>
F:1909-1941/Domain: ankyrin repeat homology <AN2>
F:1943-1975/Domain: ankyrin repeat homology <AN3>
F:1976-2008/Domain: ankyrin repeat homology <AN4>
F:2009-2041/Domain: ankyrin repeat homology <AN5>

Alignment Scores:
Pred. No.: 0.00628 Length: 2471
Score: 112.00 Matches: 38
Percent Similarity: 32.84% Conservative: 6
Best Local Similarity: 28.36% Mismatches: 37
Query Match: 12.61% Indels: 53
DB: 2 Gaps: 6

US-09-773-476-294 (1-489) x A49128 (1-2471)

QY 98 CTCAGGATGATTTGGCCACACCTTCCGTGGGTTTACTCAGCTGCAGACTCTGATACTA 157
   :: ||| ||| ||| |||
Db 912 IleAsnAspCysLeuAlaAsn----- 918

QY 158 CCACAAGATGTTCCCTGCTGGAGGTAGTAATCCCTGGGACAAATGTTACTTTTCAAG 217
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Db 919 -----ProCysGlnAsnGlySerCysValAspLysValAsnThrPheSer 934
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QY 218 -----GACAAGCAGATTTGCCAAGGGCAAGGGACCTT 250
   ||| ||| ||| ||| ::| ||| ||| |||
Db 935 CysLeuCysLeuProGlyPheValGlyAspys-----CysGlnThrAspMetAsnGlu 952
   ||| ||| ||| ||| ::| ||| ||| |||
QY 251 TGCATAGCACTGGAAGCCAGAAATGTCTCCTGAGAACGGATCTTGTGCATCTGACGGT 310
   ||| ||| ||| ||| ::| ||| ||| |||
Db 953 CysLeuSer-----GluProCysLysAsnGlyGlyThrCys---SerAspTyr 967
   ||| ||| ||| ||| ::|
QY 311 CCTGGTCTTTTGCAGTGGTTGTGCTGATGTTTCCATGCATACAAAGTGTATGAGGCAG 370
   ||| ||| ||| ||| ||| ||| ||| |||
Db 968 ValAsnSerTyrThrCysThrCysProAlaGlyPheHisGlyValHisCysGluAsnAsn 987
   ||| ||| ||| ||| ||| ||| ||| |||
QY 371 -----GGC 373

Db 988 IleAspGluCysThrGluSerSerCysPheAsnGlyGlyThrCysValAspGlyIleAsn 1007

QY 374 TCATTTTCACTGCTTATGTTCTTGGGATTTCTGGATCCA 413
   ||| ||| ||| ||| ||| ||| ||| |||
Db 1008 SerPheSer-CysLeuCysProValGlyPheThrGlyPro 1020

RESULT 3
S45306
Notch 3 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Aug-2002
C:Accession: S45306
R:Lardelli, M.; Dahlstrand, J.; Lendahl, U.
Mech. Dev. 46, 123-136, 1994
A:Title: The novel Notch homologue mouse Notch 3 lacks specific epidermal growth factor-1
A:Reference number: S45306; MUID:95001556; PMID:7918097
A:Accession: S45306
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2318 <LAR>
A:Cross-references: EMBL:X74760; NID:9483580; PID:CA452776.1; PID:9483581
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:163-195/Domain: EGF homology <EGF1>
F:474-505/Domain: EGF homology <EGF2>
F:1839-1871/Domain: ankyrin repeat homology <AN1>
F:1872-1904/Domain: ankyrin repeat homology <AN2>
F:1906-1938/Domain: ankyrin repeat homology <AN3>
F:1939-1971/Domain: ankyrin repeat homology <AN4>
F:1972-2004/Domain: ankyrin repeat homology <AN5>

Alignment Scores:
Pred. No.: 0.0488 Length: 2318
Score: 103.00 Matches: 28
Percent Similarity: 40.62% Conservative: 11
Best Local Similarity: 29.17% Mismatches: 21
Query Match: 11.60% Indels: 36
DB: 2 Gaps: 5

US-09-773-476-294 (1-489) x S45306 (1-2318)

QY 140 CTGCAGACTCTGATACACCAAGATGTTCCCTGTT----- 175
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Db 689 LeuProProLeuCysLeuProAlaAsnHisProCysAlaHisLysProCysSerHisGly 708

QY 176 -----CCTGGAGGTAGTAATGCCCTGGGACAAATGTTACTTTTCAAGGAC 220
   ||| ||| ||| ||| ||| ||| ||| |||
Db 709 ValCysHisAspAlaProGlyPheArgCys----- 719

QY 221 AAGCAGATTTGCCAA-----GGCCAAAGGGACCTTTTGCATAGCACTGGAGC 268
   ||| ||| ||| ||| ||| ||| ||| |||
Db 720 -----ValCysGluProGlyTyrSerGlyProArg-----CysSerGlnSerLeuAla 735

QY 269 CCAGAAATGTTCTCTCAG-----AACGATCTTGTGCATCTGACGGTCT 313
   ||| ||| ||| ||| ||| ||| ||| |||
Db 736 ProAspAlaCysGluSerGlnProCysGlnAlaGlyGlyThrCysThrSerAspGlyLeu 755
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A:Residues: 1-2703 <XID>  
A:Cross-references: GB:K03508; NID:gi157991; PID:AAA28725.1; PID:gi157993  
R:Wharton, K.A.; Johansen, K.M.; Xu, T.; Artavanis-Tsakonas, S.  
Cell 43, 567-581, 1985  
A:Reference number: A24768; MUID:86079539; PMID:3935325  
A:Accession: A24768  
A:Molecule type: mRNA  
A:Residues: 1-48, 'I', 50-118, 'R', 120-230, 'I', 232-256, 'N', 258-266, 'A', 268-872, 'R', 874-958, 'R', 960-1000, 'I', 1002-1003, 'R', 1005-1006, 'I', 1008-1009, 'R', 1011-1012, 'I', 1014-1015, 'R', 1017-1018, 'I', 1020-1021, 'R', 1023-1024, 'I', 1026-1027, 'R', 1029-1030, 'I', 1032-1033, 'R', 1035-1036, 'I', 1038-1039, 'R', 1041-1042, 'I', 1044-1045, 'R', 1047-1048, 'I', 1050-1051, 'R', 1053-1054, 'I', 1056-1057, 'R', 1059-1060, 'I', 1062-1063, 'R', 1065-1066, 'I', 1068-1069, 'R', 1071-1072, 'I', 1074-1075, 'R', 1077-1078, 'I', 1080-1081, 'R', 1083-1084, 'I', 1086-1087, 'R', 1089-1090, 'I', 1092-1093, 'R', 1095-1096, 'I', 1098-1099, 'R', 1101-1102, 'I', 1104-1105, 'R', 1107-1108, 'I', 1110-1111, 'R', 1113-1114, 'I', 1116-1117, 'R', 1119-1120, 'I', 1122-1123, 'R', 1125-1126, 'I', 1128-1129, 'R', 1131-1132, 'I', 1134-1135, 'R', 1137-1138, 'I', 1140-1141, 'R', 1143-1144, 'I', 1146-1147, 'R', 1149-1150, 'I', 1152-1153, 'R', 1155-1156, 'I', 1158-1159, 'R', 1161-1162, 'I', 1164-1165, 'R', 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A;Residues: 1-1722 <STO>  
A;Cross-references: GB:chr\_X; PIDN:AAC69012.1; PID:g1125776; GSPDB:GN00028; CESP:FL1C7.4  
C;Genetics:  
A;Gene: FL1C7.4  
A;Map position: X

Alignment Scores:  
Pred. No.: 100.50 Length: 1722  
Score: 100.50 Matches: 41  
Percent Similarity: 36.13% Conservative: 15  
Best Local Similarity: 26.45% Mismatches: 56  
Query Match: 11.32% Indels: 43  
DB: 2 Gaps: 6

US-09-773-476-294 (1-489) x E89753 (1-1722)

QY 46 AAACCTTTTACAGGCTTATACGCTAT-----TATCATAGACCTTCAGGCAA 93  
Db LysGlyPheSerGlyLeuLeuCysGlnAspAsnCysSerLeuHisCysLeuHisGlyAsn 67

QY 94 TCCTCTCAAGGATGATTGGCCAAACACCTT-----CCGTGGGTTTACTCA 138  
Db CysValLysGlyThrPheGlyGluThrCysGlnCysSerGluGlyTrpMetGlySer 87

QY 139 -----GCTGCACACTGTATACCTACCAAGATGTTCCCTGTCCTGGAGG 183  
Db LeuCysAspAsnLeuValThrAspAspThrAlaGlnLysCysSerProGlnCys-GI 107

QY 184 TAGTAATGCTGGACAAATGTTACTTCTTCAAGGAC---AAGCAGATTTCOCAGGCA 240  
Db YAspAsp-----GluArgCysThrLysGlyAlaAspGlySerTyrlleCysGlnSerAs 125

QY 241 AAGGACCTTTGCATAGCAGCTGGAGCCCAAAATGTCCTGAGAAGGATCTTGCC 300  
Db ngluProSerCys-----AlaThrHisThrCysGlnAsnAsnGlyThrCysVa 141

QY 301 ATCTACAGCTCTGCTTTCAGTGGCTTTGCTGATGTTTCCATGATACAAAGTG 360  
Db lalagluasn---GlyAsnValLysCysAlaCysProProGlyPheValGlyAspHisCy 160

QY 361 TATGAGG----- 367

Db sgluThrAspGluAspGluCysLysGluAsnPheCysGlnAsnGlyAlaAspCysGluAs 180

QY 368 ----CAGGCTCATTTTCACTGCTTATGTTCTTTGGGATTC 404  
Db nleuLysGlySer-tyrGluCysLysCysLeuLysGlyPhe 193

RESULT 8  
T30213  
G-cadherin - sea urchin (Lytechinus variegatus)  
C;Species: Lytechinus variegatus (variegated urchin)  
C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999  
C;Accession: T30213  
R;Miller, J.R.; McClay, D.R.  
Dev. Biol. 192, 323-339, 1997  
A;Title: Characterization of the role of cadherin in regulating cell adhesion during sea urchin gastrulation  
A;Reference number: Z20780; MUID:98104238; PMID:9441671  
A;Accession: T30213  
A;Status: preliminary; translated from GB/EMBL/DDAJ  
A;Molecule type: mRNA  
A;Residues: 1-2809 <MIL>  
A;Cross-references: EMBL:U34823; NID:g2982186; PID:g2982187; PIDN:AAC06341.1

Alignment Scores:  
Pred. No.: 0.12 Length: 2809  
Score: 99.00 Matches: 32  
Percent Similarity: 39.53% Conservative: 19  
Best Local Similarity: 24.81% Mismatches: 50  
Query Match: 11.15% Indels: 28  
DB: 2 Gaps: 5

US-09-773-476-294 (1-489) x T30213 (1-2809)

QY 158 CCACAGATGTT-----CCCTGCTCGAGGTAGTAAATCCCTGGGACAATGTT 205  
Db ProSerAspValCysAspSerAspProCysProGlySerIleLeuValCysThrAspTyr 2560

QY 206 ACTTCTTCCAGGACAGCAGATTTCACAGGCGCAAGGACCTTTGCCAATACCACTGGA 265  
Db TrpArgPheTyrGluCysLeuCysCysProGluGlyGlnGluValGluAspAspProAsp 2580

QY 266 AGC-----CCAGAAATGTTCTCTCGAGAACCGATCTTTGTGCA 301  
Db ThrCysMetAlaIleIleAspCysValProAsnProCysAlaAsnGlyGlyThrCysVal 2600

QY 302 TCTGACGCTCTGCTCTTTTTCAGTGGTTCGTCGATGGTTCATGATACCAAGTGT 361  
Db GluGlyAspProThrGlyTyrThrCysAspCysProSerGlyTyrTyrGlyAspArgCys 2620

QY 362 ATGAGGACGAGGCTCATTTTCA----- 382  
Db GluAlaAlaPheGlyGluGlnGlyAlaSerLeuGlyIleThrProLeuGlyIle 2638

QY 383 CTGCTTATGTTCTTTGGGATTCGGATCCACACGCTAGCCATCTTCATCTTCTTGG 442  
Db IleLeuMetIleLeuCysIleLeuLeuIleIleLeuLeuLeuGlyLeuValLeuTyr 2658

QY 443 GGAACCCAGCGCGGAAAGCCAAAGGCT 469  
Db ---ThrGlnArgAspArgLysSer 2666

RESULT 9  
A38261  
masking protein precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 14-Jun-1991 #sequence\_revision 14-Jun-1991 #text\_change 21-Jul-2003  
C;Accession: A38261  
R;Tsuiji, T.; Okada, F.; Yamaguchi, K.; Nakamura, T.  
Proc. Natl. Acad. Sci. U.S.A. 87, 8835-8839, 1990  
A;Title: Molecular cloning of the large subunit of transforming growth factor type beta n  
A;Reference number: A38261; MUID:91062373; PMID:2247454  
A;Accession: A38261  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1712 <TSU>  
A;Cross-references: GB:M55431; NID:g207285; PIDN:AAA42235.1; PID:g207286  
F;911-947/Domain: EGF homology <EGF>

Alignment Scores:  
Pred. No.: 0.138 Length: 1712  
Score: 98.50 Matches: 30  
Percent Similarity: 34.56% Conservative: 7  
Best Local Similarity: 28.04% Mismatches: 34  
Query Match: 11.09% Indels: 36  
DB: 2 Gaps: 4

US-09-773-476-294 (1-489) x A38261 (1-1712)

QY 164 CATGTTCCCTGCTCTCTGGAGGTAGTAAATCCCTGGGACAATGTTACTTCTTCAAGGACAAG 223  
Db 1177 AspCysThrCysProAspGlyLeuGlnLeuAsnAspAsn----- 1189

QY 224 CAGATTGCCAAGCGCAAGGACCTTTGCAATAGACTGGAAGCCCGAGAAATGTCCT 283  
Db -----LysGlyCysGlnAspIle---AsnGluCysAlaGlnProGlyLeuCysAla 1205

QY 284 GAGAACGGATCTTGTGATCTGACGGTCTCTGCTTTTTCAGTCGCTTTGTGCTGATGGT 343  
Db ProHisGlyGluCysLeuAsnThr---GlnGlySerPheHisCysValCysGlnGly 1224

QY 344 TTC----- 346  
Db PheSerIleSerAlaAspGlyArgThrCysGluAspIleAspGluCysValAsnAsnThr 1244

QY 347 -----CATGGATACAAAGTGATGATGAGGAGGCTCATTTTCACTGCTTATGTC 394

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Db 1245 ValCysAspSerHisGlyPheCysAspAsnThrAlaGlySer-PheArgCysLeuCystY 1264
QY 395 TTTGGGATTCGGGATCCA 413
Db 1264 rGlnGlyPheGlnAlaPro 1270

RESULT 10
S78549
notch3 protein - human
C:Species: Homo sapiens (man)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 08-Sep-2002
C:Accession: S78549; S71825
R:Joutel, A.; Tournier-lasserre, E.
submitted to the EMBL Data Library, April 1997
A:Reference number: S78549
A:Accession: S78549
A:Molecule type: mRNA
A:Residues: 1-2321 <JOU1>
A:Cross-references: EMBL:U97669; NID:92668591; PIDN:AA91371.1; PID:92668592
R:Joutel, A.; Corpechot, C.; Ducros, A.; Vahedi, K.; Chabrier, H.; Mouton, P.; Alamowicz, M.M.; Weissenbach, J.; Bach, J.P.; Bousser, M.G.; Tournier-lasserre, E.
Nature 383, 707-710, 1996
A:Title: Notch3 mutations in CADASIL, a hereditary adult-onset condition causing stroke
A:Reference number: S71825; MUID:97032728; PMID:8878478
A:Accession: S71825
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 67-113;138-194;268-333; 'G', 335-346;536-613;716-765;1240-1279;1815-1888 <JOU2>
A:Cross-references: EMBL:U97669
C:Genetics:
A:Gene: notch3
A:Map position: 19p13.1
C:Function:
A:Description: may be involved in pathogenesis of CADASIL, causing a type of stroke and
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
C:Keywords: tandem repeat; transmembrane protein
F:123-155/Domain: EGF homology <EGX1>
F:162-194/Domain: EGF homology <EGF1>
F:240-271/Domain: EGF homology <EGX2>
F:318-349/Domain: EGF homology <EGF>
F:473-504/Domain: EGF homology <EGX3>
F:853-884/Domain: EGF homology <EGF3>
F:928-959/Domain: EGF homology <EGX4>
F:1838-1870/Domain: ankyrin repeat homology <AN1>
F:1871-1903/Domain: ankyrin repeat homology <AN2>
F:1905-1937/Domain: ankyrin repeat homology <AN3>
F:1938-1970/Domain: ankyrin repeat homology <AN4>
F:1971-2003/Domain: ankyrin repeat homology <AN5>

Alignment Scores:
Pred. No.: 0.136 Length: 2321
Score: 98.50 Matches: 39
Percent Similarity: 30.56% Conservative: 5
Best Local Similarity: 27.08% Mismatches: 45
Query Match: 11.09% Indels: 55
DB: 2 Gaps: 5

US-09-773-476-294 (1-489) x S78549 (1-2321)
QY 52 TTTACAGCCTTACTGCTTATCATAGCTTCAGGCAATCCTCTCAAGGATGATT 111
Db 461 PheThrGlyThrTyrcys----- 466
QY 112 GGCCACACCTCCGGGGTTACTCAGCTGCAGACTGTGATCTACACACAGATGTTCC 171
Db 467 -----GluValAspIleAspGluCys-GlnSerSerPr 477
QY 172 CTGTCCTGGAGGTAGTAATCCCTGGGCAATGTTACTTCTTCAAG----- 217
Db 477 oCysValAsnGlyValCysLysAspArgValAsnGlyPheSerCysThrCysProSe 497
QY 218 -----GACACAGAGATTTCACAGGGCAAGGGACCTTTGCAATAGCACTGGAAGCCC 270

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Db 497 rGlyPheSerGlySerThrCysGlnLeuAspValAspGluCysAlaSerThr----- 514
QY 271 AGAAATGTCTCTGAGAACGGATCTTGTGCATCTGCAGGTCCTCTTTTGCAGTGGT 330
Db 515 ----ProCys---ArgAsnGlyAlaLysCysValAspGlnProAspGlyTyrgluCysAr 532
QY 331 TTCTGCTGATGGTTTCCATGATACAGTCTATAGGCAG----- 370
Db 532 gCysAlaGluGlyPheGluGlyThrLeuCysAspArgAsnValAspAspCysSerProAs 552
QY 371 -----GGCTCATTTTCACCTGCCTATGTTCTT 396
Db 552 pProCysHisHisGlyArgCysValAspGlyIleAlaSerPheSer-CysAlaCysAlaP 572
QY 397 TGGGATTC 404
Db 572 roGlyTyrcys----- 574

RESULT 11
S18188
notch protein homolog - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
C:Accession: S18188
R:Weinmaster, G.; Roberts, V.J.; Lemke, G.
Development 113, 199-205, 1991
A:Title: A homolog of Drosophila Notch expressed during mammalian development.
A:Reference number: S18188; MUID:92111383; PMID:1764995
A:Accession: S18188
A:Molecule type: mRNA
A:Residues: 1-2531 <WEI>
A:Cross-references: EMBL:X57405; NID:957634; PID:957635
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:987-1018/Domain: EGF homology <EGF1>
F:1025-1056/Domain: EGF homology <EGF2>
F:1233-1264/Domain: EGF homology <EGF2>
F:1917-1949/Domain: ankyrin repeat homology <AN1>
F:1950-1982/Domain: ankyrin repeat homology <AN2>
F:1984-2016/Domain: ankyrin repeat homology <AN3>
F:2017-2049/Domain: ankyrin repeat homology <AN4>
F:2050-2082/Domain: ankyrin repeat homology <AN5>

Alignment Scores:
Pred. No.: 0.151 Length: 2531
Score: 98.00 Matches: 41
Percent Similarity: 33.95% Conservative: 14
Best Local Similarity: 25.31% Mismatches: 56
Query Match: 11.04% Indels: 51
DB: 2 Gaps: 8

US-09-773-476-294 (1-489) x S18188 (1-2531)
QY 53 TTACAGGCTTATCTGCT-----ATTATCATAGACCTTCAG-----GCAATCCT 97
Db 441 LeuGlnGlyTyrcysGlyProArgCysGluIleAspValAsnGluCysIleSerAsnPro 460
QY 98 CTCAGAGGATGATTGGCCACACCTTCGGGGTTTACTCAGCTGCAGCTCTGATCTACTA 157
Db 461 CysGlnAsnAsp---AlaThrCysLeuAspGlnIleGlyGluPheGlnCysIleCysMet 479
QY 158 CCA-----CAAGATGTTCCCTGT 175
Db 480 ProGlyTyrcysGluGlyValTyrcysGluIleAsnThrAspGluCysAlaSerProCys 499
QY 176 CTGGAGGTAGTAATGCTGGACAATGTTACTTCTTCAAG----- 217
Db 500 LeuHisAsnGlyArgCysValAspLysIleAsnGluPheLeuCysGlnCysProLysGly 519
QY 218 ---GACACAGCAGATTTCGCAAGGGCAAGGACCTTTGCAATAGCACTGGAAGCCCAGAA 274
Db 520 PheSerGlyHisLeuCysGlnTyrcysValAspValAspGluCysAlaSerThr----- 535

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QY	275	ATGTGTCCTGAGAACGGATCTTTGTGCATCTGACGGCTCTCGTCTCTTTTGCAGTACGCTTTGT	334
		:  :    :	
Db	536	ProCys---LysAsnGlyAlaLysCysLeuAspGlyProAsnThrTyrThrCysValCys	554
		:  :    :	
QY	335	GCTGATGTTTCCATGGATACAAAGTGT-	361
		:  :    :	
Db	555	ThrGluGlyTyrThrGlyThrHisCysGluValAspLeuAspGluCysAspProAspPro	574
		:  :    :	
QY	362	-----ATGAGCAGGGCTCATTTCACTGCTTTATGTTCTTTTGGG	400
		:  :    :	
Db	575	CysHisIleGlyLeuCysLysAsp-GlyValAlaIaThrPheThrCysLeuCysGlnProGln	594
		:  :    :	
QY	401	ATTC 404	
		:  :    :	
Db	594	Ytyr 595	
		:  :    :	
RESULT 12			
T09059			
notch4 - mouse			
C;Species: Mus musculus (house mouse)			
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 08-Sep-2002			
C;Accession: T09059			
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Lorentz, L.; et al. 1997			
A;Submitted to the EMBL Data Library, October 1997			
A;Description: Sequence of the mouse major histocompatibility locus class III			
A;Reference number: Z16543			
A;Accession: T09059			
A;Status: Preliminary; translated from GB/EMBL/DBJ			
A;Molecule type: DNA			
A;Residues: 1-1964 <ROW>			
A;Cross-references: EMBL:AF030001; NID:g2564945; PID:g2564947			
C;Genetics:			
A;Gene: notch4			
A;Map position: 17			
A;Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1;			
1679/3; 1729/1; 1762/3			
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology			
C;Keywords: receptor; signal transduction			
F;514-545/Domain: EGF homology <EGF>			
Alignment Scores:			
Pred. No.: 0.172	Length: 1964		
Score: 97.50	Matches: 34		
Percent Similarity: 34.68%	Conservative: 9		
Best Local Similarity: 27.42%	Mismatches: 43		
Query Match: 10.98%	Indels: 38		
DB: 2	Gaps: 6		
US-09-773-476-294 (1-489) x T09059 (1-1964)			
QY	128	GGGTTTACTCAGCTCGAGACTCTGATCTACACACAGATGTT-----CCCTGCTCT 178	
		:  :    :	
Db	264	GlyPheThrGlyLeuAspCysGluMetAsnProAspAspCysValArgHisGlnCysGln 283	
		:  :    :	
QY	179	GGAGGTAGTAAATGCCCTGGGACAAATGTTACTCTTTTCAAG----- 217	
		:  :    :	
Db	284	AsnGlyAlaThrCysLeuAspGlyLeuAspThrTyrThrCysLeuCysProLysThrTrp 303	
		:  :    :	
QY	218	-----GACAAAGCAGATTTGCCAAGGCGAAGGACCTTTGCAATAGCACTGGAAGC 268	
		:  :    :	
Db	304	LysGlyTrpAsp-----CysSerGluAspIleAspGluCysGluAlaArgGlyPro 320	
		:  :    :	
QY	269	CCGAAATGTCTCTGAGAACGGAATCTTGTGCATCTGACGGTCTCTTTTGCAGTGC 328	
		:  :    :	
Db	321	ProArg---CysArgAsnGlyGlyThrCysGlnAsnThrAla---GlySerPheHisCys 338	
		:  :    :	
QY	329	GTTTGTCTCATGGTTTCCATGGATACAAAGTGTATG----- 364	
		:  :    :	
Db	339	ValCysValSerGlyTrpGlyGlyAlaGlyCysGluGluAsnLeuAspAspCysAlaAla 358	
		:  :    :	
QY	365	-----AGGCAGGGCTCATTTTCACTGCTTATG 391	
		:  :    :	
Db	359	AlaThrCysAlaProGlySerThrCysIleAspArgValGlySerPheSer-CysLeuCy 378	
		:  :    :	

Qy 392 TTCTTTGGGA 401  
Db 378 sProProGly 381

RESULT 13

A54785

Preadipocyte factor 1 precursor, long form - mouse

N:Alternate names: delta-like dlk homeotic protein; pref-1

C:Species: Mus musculus (house mouse)

C:Date: 12-Apr-1995 #sequence\_revision 12-Apr-1995 #text\_change 02-Aug-2002

C:Accession: A54785; A45484; A40746; S21585

R:Smas, C.M.; Green, D.; Sul, H.S.

Biochemistry 33, 9257-9265, 1994

A:Title: Structural characterization and alternate splicing of the gene encoding the preadipocyte factor 1 precursor, long form

A:Reference number: A54785; MUID:94325292; PMID:7519443

A:Accession: A54785

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-385 <SMA>

A:Cross-references: GB:S71340

R:Laborda, J.; Sauville, E.A.; Hoffman, T.; Notario, V.

J. Biol. Chem. 269, 3917-3920, 1993

A:Title: dlk, a putative mammalian homeotic gene differentially expressed in small cell lung carcinoma

A:Reference number: A45484; MUID:93179372; PMID:8095043

A:Accession: A45484

A:Molecule type: mRNA

A:Residues: 1-78,'G','80-343','TP','346-385 <LAB>

A:Cross-references: EMBL:J21171; NID:G50716; PIDN:CAA78162.1; PID:G50717

A:Note: sequence extracted from NCBI backbone (NCBIP:125734)

A:Note: species designations for this sequence report and for B45484 originally were tra

R:Smas, C.M.; Sul, H.S.

Cell 73, 725-734, 1993

A:Title: Pref-1, a protein containing EGF-like repeats, inhibits adipocyte differentiation

A:Reference number: A40746; MUID:93272313; PMID:8500166

A:Accession: A40746

A:Molecule type: mRNA

A:Residues: 1-78,'G','80-249','P','251-319,'CWAPWPSFSSTSAKPGCTCATTCFARRRTCCSITAAKSWRSISG

A:Cross-references: GB:J12721; MID:G303092; PIDN:AAA37175.1; PID:G309093

A:Experimental source: 3T3-L1 preadipocytes

A:Note: this sequence appears to have been corrected in reference A45484

C:Superfamily: preadipocyte factor 1; EGF homology

C:Keywords: alternative splicing; tandem repeat; transmembrane protein

F:1-385/Product: preadipocyte factor 1 precursor splice form A #status predicted <FOA>

F:1-230/282-385/Product: preadipocyte factor 1 precursor splice form B #status predicted

F:1-230/304-385/Product: preadipocyte factor 1 precursor splice form C #status predicted

F:1-230/306-385/Product: preadipocyte factor 1 precursor splice form D #status predicted

F:1-210/304-385/Product: preadipocyte factor 1 precursor splice form D #status predicted

F:1-210/306-385/Product: preadipocyte factor 1 precursor splice form D2 #status predicted

F:92-124/Domain: EGF homology <EGF>

F:214-246/Domain: EGF homology <EGF1>

Alignment Scores:			
Pred. No.:	0.301	Length:	385
Score:	95.50	Matches:	33
Percent Similarity:	30.3%	Conservative:	8
Best Local Similarity:	24.4%	Mismatches:	45
Query Match:	10.75%	Indels:	49
DB:	2	Gaps:	4

US-09-773-476-294 (1-489) x A54785 (1-385)

Qy 133 TACTCAGCTGCAGACTCTGATACTACCAAGATGTTCCCTGCTGAGGTACTAATGC 192

Db 34 TyrGlyPheCysGluAlaAspAsnValCysArgCysHisValGlyTrpGluGlyProLeu 53

Qy 193 CTGGGACATGTACTCTTCAAGGA-----CAA 222

Db 54 CysAspLysCysValThrAlaProGlyCysValAsnGlyValCysLysGluProTrpGln 73

Qy 223 GCAGATTTTGCCAAAGGCCAAAGGAC-----CATTGCAA 255

Db 74 Cys-IleCysIleAspGlnTrpAspGlyLysPheCysGluIleAspValArgAlaCysTh 93  
 QY 256 TAGCAGTGGAGCCAGAAATGCTCTGAGAACGGATCTTGTCATCTGACGGTCTCTG 315  
 Db 93 rSerThr-----ProCysAlaAsnAsnGlyThrCysValAspLeuGluLysG 109  
 QY 316 TCCTTTGACAGTGGCTTTGCTGCTGATGTTTCCATGATACAAAGTGTATGAGGAGGGCT- 374  
 Db 109 YGlnTyrGluCysSerCysThrProGlyPheSerGlyLysAspCysGlnHis-LysAlaG 129  
 QY 374 ----- 374  
 Db 129 lyProCysValIleAsnGlySerProCysGlnHisGlyAlaCysValAspAspGluG 149  
 QY 375 -----CATTTTCACTGGCTTATGTTCTTTTGGGATTC 404  
 Db 149 lyGlnAlaSerHisAlaSerCysLeuCysProProGlyPhe 162

RESULT 14  
 A35626  
 transforming growth factor beta-1-binding protein - human  
 C:Species: Homo sapiens (man)  
 C>Date: 21-Sep-1990 #sequence\_revision 21-Sep-1990 #text\_change 21-Jul-2003  
 C:Accession: A35626  
 R:Kanzaki, T.; Olofsson, A.; Moren, A.; Wernstedt, C.; Hellman, U.; Miyazono, K.; Claess  
 Cell 61, 1051-1061, 1990  
 A>Title: TGF-beta1 binding protein: a component of the large latent complex of TGF-beta1  
 A:Reference number: A35626; PMID:90275601; PMID:2350783  
 A:Accession: A35626  
 A>Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-1394 <N>  
 A:Cross-references: GB:M34057; NID:G339547; PIDN:AAA61160.1; PID:G339548  
 C:Keywords: alternative splicing  
 F:750-791/Domain: EGF homology <EGF>

Alignment Scores:  
 Pred. No.: 0.277 Length: 1394  
 Score: 95.50 Matches: 31  
 Percent Similarity: 31.78% Conservative: 3  
 Best Local Similarity: 28.97% Mismatches: 37  
 Query Match: 10.75% Indels: 36  
 DB: 2 Gaps: 4

US-09-773-476-294 (1-489) x A35626 (1-1394)  
 QY 164 GATGTTCCCTGCTCTGGAGTAGTAATGCTGGCAATGTTACTTCTTTCAAGGACAAG 223  
 Db 858 AspCysThrCysProAspGlyPheGlnLeuAspAspAsnLysThr----- 872  
 QY 224 CAGATTGCGCAAGGCAAGGACCTTTCATAGCACTGGAGCCGACCAATGTGCTCT 283  
 Db 873 -----CysGlnAsp-----IleAsnGluCysGluHisProGlyLeuCysGly 886  
 QY 284 GAGAACGGATCTTTCATCTGACGCTCTGCTGCTTTTTCAGTGGCTTTGCTGCTGATG 343  
 Db 887 ProGlnGlyCysLeuAsnThr-----GluGlySerPheHisCysValCysGlnGlnGly 905  
 QY 344 TTC----- 346  
 Db 906 PheSerIleSerAlaAspGlyArgThrCysGluAspIleAspGluCysValAsnAsnThr 925  
 QY 347 -----CATGGATACAAAGTGTATGACGAGCGGCTCATTTTCACTGCTTATGTTTC 394  
 Db 926 ValCysAspSerHisGlyPheCysAspAsnThrAlaGlySer-PheArgCysLeuCysTy 945  
 QY 395 TTGGGATTCGGATCCA 413  
 Db 945 rGlnGlyPheGlnAlaPro 951

RESULT 15

T29234

hypothetical protein F55G1.13 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T29234  
 R:Murray, J.; Le, T.T.  
 submitted to the EMBL Data Library, May 1996  
 A:Description: The sequence of C. elegans cosmid F55G1.  
 A:Reference number: Z20591  
 A:Accession: T29234  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-616 <MUR>  
 A:Cross-references: EMBL:U58750; PIDN:AA00653.1; GSPDB:GN00022; CESP:F55G1.13  
 A:Experimental source: strain Bristol N2; clone F55G1  
 C:Genetics:  
 A:Gene: CESP:F55G1.13  
 A:Map position: 4  
 A:Introns: 98/1; 136/1; 230/1; 256/1; 363/1; 401/1; 443/1; 484/1; 528/2; 551/3

Alignment Scores:  
 Pred. No.: 0.327 Length: 616  
 Score: 95.00 Matches: 36  
 Percent Similarity: 38.71% Conservative: 12  
 Best Local Similarity: 29.03% Mismatches: 43  
 Query Match: 10.70% Indels: 33  
 DB: 2 Gaps: 6

US-09-773-476-294 (1-489) x T29234 (1-616)  
 QY 64 TACTGCTATTATCATAGACCTTCAGGCAATCCTCTCAAGGATGATTTGGCCACACCTT 123  
 Db 28 TyrCysTyr-----ProAlaAsnArgThrSerAlaThrThrCysSerGluCysThr 44  
 QY 124 CCGTGGGTTTACTCAGCTGCAGCTCTGTACTACTACC----- 159  
 Db 45 CysSerAspGluSerThrGlnThrSerAspThrThrCysThrAlaProThrSerCysSer 64  
 QY 160 ---ACAAGATGTTCCCTGCTCTGGAGGTAGTAATGCTGGGAGCAATGTTACTTCTTCAA 216  
 Db 65 ProAsnProCysThrLeuSerAsnGln-----GlnCysAsnMetValAsn 79  
 QY 217 GGACAAGCAGATTTCACAGGGCAAGGGACCTTTCATAGCACTGGA----- 265  
 Db 80 -----AspIleProThrCysThrCysAlaVal-GlyTyr-ThrGlyThrAspCysTh 96  
 QY 266 -----AGCCCAAGAAATGTCTCTGAGAACGGATCTTGTGATC 303  
 Db 96 rMetLeuThrSerAspProCysSerProGlnProCysLeuGlnAsnGlyValCysSerSe 116  
 QY 304 TGACGGTCCCTGGCTTTTTCAGTGGCTTTGCTGATGGTTTCCATGGATACAAAGTGTAT 363  
 Db 116 rSerGly--GlyThrTyrSerCysAlaCysAlaThrGlyPhePheGlyGluGlnCysG 135  
 QY 364 GAGCCAGGGC 373  
 Db 135 nTyrSerGly 138

Search completed: June 25, 2004, 09:17:56

Job time : 26 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 25, 2004, 09:09:32 ; Search time 14 Seconds  
(without alignments)  
3637.472 Million cell updates/sec

Title: US-09-773-476-294

Perfect score: 888  
Sequence: 1 gactgaggctagattcttcag.....tnatgagccacacaaagactt 489

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Dalext 7.0

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 283362

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame\_n2p.model -DEV=xlp  
-Q/cgn2\_1/USProt\_42 -QPMI=fastan -SUFFIX=n2p.rsp -MINMATCH=0.1 -LOOPEL=0  
-LOOPEXT=0 -UNITS=bits -SPART=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORW=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09773476 @CGN 1.16 @runat 25062004.090846 5816 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT\_DSBLCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPEXT=10 -XGAPOP=6  
-XGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	113	12.7	2470	1 NTC2_MOUSE	O35516 mus musculus
2	112	12.6	2471	1 NTC2_RAT	Q9q30 rattus norv
3	103	11.6	2318	1 NTC3_MOUSE	Q61982 mus musculus
4	103	11.6	2531	1 NTC1_MOUSE	Q01705 mus musculus
5	102	11.5	2471	1 NTC2_HUMAN	Q04721 homo sapien
6	102	11.5	2703	1 NOTC_DROME	P07207 drosophila
7	101	11.4	2556	1 NTC1_HUMAN	P46531 homo sapien
8	100	11.3	2319	1 NTC3_RAT	Q9r172 rattus norv
9	99	11.1	1213	1 JAG3_BRARE	Q9y54 brachydanio
10	99	11.1	1964	1 NTC4_MOUSE	P31695 mus musculus
11	99	11.1	2003	1 NTC4_HUMAN	Q99466 homo sapien
12	98.5	11.1	1389	1 LTBS_MOUSE	Q8CG18 mus musculus
13	98.5	11.1	1712	1 LTBI_RAT	Q00818 rattus norv
14	98.5	11.1	1713	1 LTBL_MOUSE	Q8CG19 mus musculus
15	98.5	11.1	2321	1 NTC3_HUMAN	Q9um47 homo sapien
16	98	11.0	2531	1 NTC1_RAT	Q07008 rattus norv
17	96.5	10.9	1242	1 JAG1_BRARE	Q90y57 brachydanio
18	95.5	10.8	1394	1 LTBS_HUMAN	P22064 homo sapien

19	95.5	10.8	1595	1 LTBL_HUMAN	Q14766 homo sapien
20	95	10.7	675	1 PRIS_RAT	P53813 rattus norv
21	95	10.7	4391	1 PGEM_HUMAN	P98160 homo sapien
22	94.5	10.6	1218	1 JAG1_MOUSE	Q9qxx0 mus musculus
23	94.5	10.6	1219	1 JAG1_RAT	Q63722 rattus norv
24	94.5	10.6	2437	1 NTC1_BRARE	P46530 brachydanio
25	94	10.6	383	1 DLK_HUMAN	P80370 homo sapien
26	93.5	10.5	1218	1 JAG1_HUMAN	P78504 homo sapien
27	92.5	10.4	1238	1 JAG2_HUMAN	Q9y219 homo sapien
28	92.5	10.4	2524	1 NOTC_XENLA	P21783 xenopus lae
29	92.5	10.4	2907	1 FBN2_MOUSE	Q61555 mus musculus
30	92.5	10.4	2911	1 FBN2_HUMAN	P35556 homo sapien
31	92.5	10.4	4544	1 LRPI_HUMAN	Q07954 homo sapien
32	91.5	10.3	705	1 FBLL_MOUSE	Q08879 mus musculus
33	91.5	10.3	1202	1 JAG2_RAT	P97607 rattus norv
34	91.5	10.3	1247	1 JAG2_MOUSE	Q9q58 mus musculus
35	91	10.2	1408	1 SERR_DROME	P18168 drosophila
36	89.5	10.1	473	1 FP2_MYTGA	Q25464 mytilus gal
37	89	10.0	1064	1 FBPI_STRPU	P10079 strongyloce
38	89	10.0	2871	1 FBNI_PIG	Q9tv36 sus scrofa
39	88.5	10.0	385	1 DLK_MOUSE	Q09163 mus musculus
40	88.5	10.0	598	1 FBLL_CERAE	Q8mj39 cercopithec
41	88.5	10.0	1799	1 LMB2_MOUSE	Q61392 mus musculus
42	87.5	9.9	704	1 FBLL_CHICK	O73775 gallus gall
43	87	9.8	2871	1 FBNI_BOVIN	P98133 bos taurus
44	87	9.8	2871	1 FBNI_HUMAN	P35555 homo sapien
45	87	9.8	2871	1 FBNI_MOUSE	Q61554 mus musculus

#### ALIGNMENTS

RESULT 1  
NTC2\_MOUSE  
ID NTC2\_MOUSE STANDARD; PRT; 2470 AA.  
AC O35516; Q06008; Q60941;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neurogenic locus notch homolog protein 2 precursor (Notch 2) (Motch  
B).  
GN NOTCH2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Thymus;  
RA Hamada Y., Higuchi M., Tsujimoto Y.;  
RT "Complete amino acid sequence and multiform transcripts encoded by a  
single copy of mouse Notch2 gene."  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 316-1518 FROM N.A.  
RC STRAIN=C57BL/6 X CBA; TISSUE=Embryo;  
RA MEDLINE=93178563; PubMed=8440332;  
RX Lardelli M., Lendahl U.;  
RT "Motch A and Motch B-two mouse Notch homologues coexpressed in a  
wide variety of tissues."  
RL Exp. Cell Res. 204:364-372(1993).  
RN [3]  
RP SEQUENCE OF 1765-2153 FROM N.A.  
RX MEDLINE=97075110; PubMed=8917536;  
RA Milner L.A., Bigas A., Kopan R., Brashem-Stein C., Bernstein I.D.,  
RT Martin D.I.;  
RT "Inhibition of granulocytic differentiation by mNotch1."  
RL Proc. Natl. Acad. Sci. U.S.A. 93:13014-13019(1996).  
RN [4]  
RP FUNCTION  
RX MEDLINE=99396706; PubMed=10393120;  
RA Hamada Y., Kadohawa Y., Okabe M., Ikawa M., Coleman J.R.,  
RT Tsujimoto Y.;  
RT "Mutation in ankyrin repeats of the mouse Notch2 gene induces early

embryonic lethality.";  
Development 126:3415-3424 (1999).  
[5]  
RX DEVELOPMENTAL STAGE, AND ALTERNATIVE SPLICING.  
RX MEDLINE=95333893; PubMed=7609614;  
RA Higuchi M., Kiyama H., Hayakawa T., Hanada Y., Tsujimoto Y.;  
PT "Differential expression of Notch1 and Notch2 in developing and adult  
mouse brain.";  
RL Brain Res. Mol. Brain Res. 29:263-272 (1995).  
[6]  
RX POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699.  
RX MEDLINE=21523956; PubMed=11518718;  
RA Saxena M.T., Schroter E.H., Mumm J.S., Kopan R.;  
PT "Murine notch homologs (N1-4) undergo presenilin-dependent  
proteolysis.";  
RL J. Biol. Chem. 276:40268-40273 (2001).  
[7]  
RX POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699.  
RX MEDLINE=21374376; PubMed=11459941;  
RA Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;  
PT "Conservation of the biochemical mechanisms of signal transduction  
among mammalian Notch family members.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031 (2001).  
CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands  
Jagged1, Jagged2 and Deltal to regulate cell-fate determination.  
Upon ligand activation through the released notch intracellular  
domain (NICD) it forms a transcriptional activator complex with  
RBP-J kappa and activates genes of the enhancer of split locus.  
Affects the implementation of differentiation, proliferation and  
apoptotic programs (By similarity). May play an essential role in  
postimplantation development, probably in some aspect of cell  
specification and/or differentiation.  
CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-  
terminal fragment N(EC) which are probably linked by disulfide  
bonds.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following  
proteolytical processing NICD is translocated to the nucleus.  
CC -!- ALTERNATIVE PRODUCTS:  
Event=Alternative splicing; Named isoforms=2;  
Names=1;  
IsoId=O35516-1; Sequence=Displayed;  
Names=2;  
IsoId=O35516-2; Sequence=VSP\_001405;  
Note=No experimental confirmation available;  
CC -!- TISSUE SPECIFICITY: Expressed in the brain, liver, kidney,  
neuroepithelia, somites, optic vesicles and branchial arches, but  
not heart.  
CC -!- DEVELOPMENTAL STAGE: Expressed in the embryonic ventricular zone,  
the postnatal ependymal cells, and the choroid plexus throughout  
embryonic and postnatal development.  
CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form  
which is proteolytically cleaved by a furin-like convertase in the  
trans-Golgi network before it reaches the plasma membrane to yield  
an active, ligand-accessible form. Cleavage results in a C-  
terminal fragment N(TM) and a N-terminal fragment N(EC). Following  
ligand binding, it is cleaved by TNF-alpha converting enzyme  
(TACE) to yield a membrane-associated intermediate fragment called  
notch extracellular truncation (NEXT). This fragment is then  
cleaved by presenilin dependent gamma-secretase to release a  
notch-derived peptide containing the intracellular domain (NICD)  
from the membrane.  
CC -!- PTM: Phosphorylated.  
CC -!- SIMILARITY: Belongs to the NOTCH family.  
CC -!- SIMILARITY: Contains 35 EGF-like domains.  
CC -!- SIMILARITY: Contains 2 lin/Notch repeats.  
CC -!- SIMILARITY: Contains 6 ANK repeats.  
CC  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
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CC EMBL; D32210; BAA22094.1; -;  
CC EMBL; X68279; CAA48340.1; -;  
DR EMBL; U31881; AAC52924.1; -;  
DR PIR; A49175; A49175.  
DR HSSP; P16109; 1FSB.  
DR MGD; MGI:97364; Notch2.  
DR GO; GO:0005887; C:integral to plasma membrane; IC.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0002011; P:morphogenesis of an epithelial sheet; IMP.  
DR GO; GO:0007219; P:N signaling pathway; IC.  
DR InterPro; IPR002110; ANK.  
DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001981; EGF\_Ca.  
DR InterPro; IPR001438; EGF\_II.  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR002049; Laminin\_EGF.  
DR InterPro; IPR008297; Notch\_dom.  
DR InterPro; IPR000800; Notch\_dom.  
DR Pfam; PF00023; ank; 6.  
DR Pfam; PF00008; EGF; 34.  
DR Pfam; PF00066; notch; 2.  
DR PIRSF; PIRSF002279; Notch; 1.  
DR PRINTS; PR00010; EGFLOOD.  
DR PRINTS; PR00011; EGFELAMININ.  
DR PRINTS; PR01452; NOTCH.  
DR SMART; SM00248; ANK; 6.  
DR SMART; SM00179; EGF\_CA; 23.  
DR SMART; SM00004; NL; 3.  
DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
DR PROSITE; PS50088; ANK\_REPEAT; 4.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 22.  
DR PROSITE; PS00022; EGF\_1; 33.  
DR PROSITE; PS01186; EGF\_2; 27.  
DR PROSITE; PS50026; EGF\_3; 35.  
DR PROSITE; PS01187; EGF\_CA; 22.  
KW Receptor; Transcription regulation; Activator; Differentiation;  
KW Developmental protein; Repeat; ANK repeat; EGF-like domain;  
KW Transmembrane; Glycoprotein; Signal; Phosphorylation;  
KW Alternative splicing.  
FT SIGNAL 1 25  
FT CHAIN 26 2470 POTENTIAL.  
FT CHAIN 1666 2470 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 2.  
FT CHAIN 1697 2470 NOTCH EXTRACELLULAR TRUNCATION.  
FT CHAIN 26 1677 NOTCH INTRACELLULAR DOMAIN.  
FT DOMAIN 26 1677 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 1678 1698 POTENTIAL.  
FT DOMAIN 1699 2470 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 26 63 EGF-LIKE 1.  
FT DOMAIN 64 102 EGF-LIKE 2.  
FT DOMAIN 105 143 EGF-LIKE 3.  
FT DOMAIN 144 180 EGF-LIKE 4.  
FT DOMAIN 182 219 EGF-LIKE 5; CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 221 256 EGF-LIKE 6 (INCOMPLETE).  
FT DOMAIN 258 294 EGF-LIKE 7; CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 296 334 EGF-LIKE 8; CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 336 372 EGF-LIKE 9; CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 373 411 EGF-LIKE 10.  
FT DOMAIN 413 452 EGF-LIKE 11; CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 454 490 EGF-LIKE 12; CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 492 528 EGF-LIKE 13; CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 530 566 EGF-LIKE 14; CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 568 603 EGF-LIKE 15; CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 605 641 EGF-LIKE 16; CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 643 678 EGF-LIKE 17; CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 680 716 EGF-LIKE 18; CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 718 753 EGF-LIKE 19.  
FT DOMAIN 755 791 EGF-LIKE 20; CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 793 829 EGF-LIKE 21; CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 831 869 EGF-LIKE 22.  
FT DOMAIN 871 907 EGF-LIKE 23; CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 909 945 EGF-LIKE 24; CALCIUM-BINDING (POTENTIAL).  
CC

FT DOMAIN 947 983 EGF-LIKE 25, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 985 1021 EGF-LIKE 26, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 1023 1059 EGF-LIKE 27, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 1061 1097 EGF-LIKE 28.  
FT DOMAIN 1099 1145 EGF-LIKE 29.  
FT DOMAIN 1147 1183 EGF-LIKE 30, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 1185 1221 EGF-LIKE 31, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 1223 1260 EGF-LIKE 32, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 1262 1300 EGF-LIKE 33.  
FT DOMAIN 1302 1345 EGF-LIKE 34.  
FT DOMAIN 1372 1410 EGF-LIKE 35.  
FT REPEAT 1418 1454 LIN/NOTCH 1.  
FT REPEAT 1501 1533 LIN/NOTCH 2.  
FT REPEAT 1825 1869 ANK 1.

Alignment Scores:  
Score: 0.0012 Length: 2470  
PId: 113.00 Matches: 38  
Percent Similarity: 33.58% Conservative: 7  
Best Local Similarity: 28.36% Mismatches: 36  
Query Match: 12.73% Indels: 53  
DB: 1 Gaps: 6

US-09-773-476-294 (1-489) x NTC2\_MOUSE (1-2470)  
QY 98 CTCAGGATGATTGGCCACACCTTCGCTGGGTTTACTCAGTCGAGACTCTGACTA 157  
DB 910 lIleAsnAspCysLeuAlaAsn----- 916  
QY 158 CCACAAGATGTCCTCTCTCGAGGTAGTATGCTCGGGACAATGTTACTTCTTCAAG 217  
DB 917 -----ProCysGlnAsnGlySerCysValAspHisValAsnThrPheSer 932  
QY 218 -----CACACAGCAGATTGCCAAGGGCAAGGACCTT 250  
DB 933 CysGlnCysHisProGlyPheIleGlyAspLys-----CysGlnThrAspMetAsnGlu 950  
QY 251 TGCATATGACATGGAGCCCAAGATGTCTCTGAGACGATCTGTGCAATCTGACGGT 310  
DB 951 CysLeuSer-----GluProCysLysAsnGlyGlyThrCys---SerAspTyr 965  
QY 311 CTGGTCTTTTGCAGTGGTTGTCTGATGTTTCCATGGATACAACTGTATGAGCGAC 370  
DB 966 ValAsnSerTyrThrCysThrCysProAlaGlyPheHisGlyValHisCysGluAsnAsn 985  
QY 371 -----GGC 373  
DB 986 lIleAspGluCysThrGluSerSerCysPheAsnGlyGlyThrCysValAspGlyLeuAsn 1005  
QY 374 TCATTTTCACTCTATGTTCTTTGGGATCTGGGATCCA 413  
DB 1006 SerPheSer-CysLeuCysProValGlyPheThrGlyPro 1018

RESULT 2  
NTC2\_RAT  
ID NTC2\_RAT STANDARD; PRT; 2471 AA.  
AC Q9W30;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neurogenic locus notch homolog protein 2 precursor (Notch 2).  
GN NOTCH2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=93302015; PubMed=1295745;  
RA Weinmaster G., Roberts V.J., Lemke G.;  
RT "Notch2: a second mammalian Notch gene.";  
RL Development 116:931-941(1992).

[2]  
RN TISSUE SPECIFICITY.  
RP MEDLINE=21331789; PubMed=11438922;  
RX Irvin D.K., Zurcher S.D., Nguyen T., Weinmaster G., Kornblum H.I.;  
RA "Expression patterns of Notch1, Notch2, and Notch3 suggest multiple functional roles for the Notch-DSL signaling system during brain development.";  
RT J. Comp. Neurol. 436:167-181(2001).  
CC -I- FUNCTION: Functions as a receptor for membrane-bound ligands Jagged1, Jagged2 and Deltal to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs. May play an essential role in postimplantation development, probably in some aspect of cell specification and/or differentiation (By similarity).  
CC -I- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide bonds (By similarity).  
CC -I- SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus.  
CC -I- TISSUE SPECIFICITY: Highly expressed in the spleen and choroid plexus in the brain. Expressed in postnatal central nervous system (CNS) germinal zones and, in early postnatal life, within numerous cells throughout the CNS. It is more highly localized to ventricular germinal zones. Also found in the heart, liver and kidney.  
CC -I- DEVELOPMENTAL STAGE: Expressed in the brain during E14 and E17.  
CC -I- PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presenilin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane (By similarity).  
CC -I- PTM: Phosphorylated (By similarity).  
CC -I- SIMILARITY: Belongs to the NOTCH family.  
CC -I- SIMILARITY: Contains 35 EGF-like domains.  
CC -I- SIMILARITY: Contains 2 lin/Notch repeats.  
CC -I- SIMILARITY: Contains 6 ANK repeats.  
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CC EMBL; M93661; AAK13558.1; -.  
CC PIR; A49128; A49128.  
CC HSSP; P00743; ICCF.  
DR InterPro; IPR002110; ANK.  
DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR000742; EGF 2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001438; EGF\_II.  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR002049; Laminin\_EGF.  
DR InterPro; IPR008297; Notch.  
DR InterPro; IPR008000; Notch\_dom.  
DR Pfam; PF00023; ank; 6.  
DR Pfam; PF00008; EGF; 35.  
DR Pfam; PF00066; notch; 2.  
DR PIRSF; PIRSF002279; Notch; 1.  
DR PRINTS; PR00010; EGF\_BLOOD.  
DR PRINTS; PR00011; EGFLAMININ.  
DR PRINTS; PR01452; NOTCH.

DR	SMART; SMO0248; ANK; 6.	90	FT	DISULFID	73	101	BY SIMILARITY.
DR	SMART; SMO0179; EGF CA; 24.	101	FT	DISULFID	92	101	BY SIMILARITY.
DR	SMART; SMO0004; NL; 2.	121	FT	DISULFID	109	121	BY SIMILARITY.
DR	PROSITE; PS00297; ANK_REPEAT; 1.	131	FT	DISULFID	115	131	BY SIMILARITY.
DR	PROSITE; PS00088; ANK_REPEAT; 4.	142	FT	DISULFID	133	142	BY SIMILARITY.
DR	PROSITE; PS00010; ASX_HYDROXYL; 22.	159	FT	DISULFID	148	159	BY SIMILARITY.
DR	PROSITE; PS00022; EGF_1; 34.	168	FT	DISULFID	153	168	BY SIMILARITY.
DR	PROSITE; PS01185; EGF_2; 26.	179	FT	DISULFID	170	179	BY SIMILARITY.
DR	PROSITE; PS00026; EGF_3; 35.	186	FT	DISULFID	186	186	BY SIMILARITY.
DR	PROSITE; PS01187; EGF CA; 22.	207	FT	DISULFID	192	207	BY SIMILARITY.
KW	Receptor; Transcription regulation; Activator; Differentiation;	218	FT	DISULFID	209	218	BY SIMILARITY.
KW	Developmental protein; Repeat; ANK repeat; EGF-like domain;	236	FT	DISULFID	225	236	BY SIMILARITY.
KW	Transmembrane; Glycoprotein; Signal; Phosphorylation.	246	FT	DISULFID	230	246	BY SIMILARITY.
FT	SIGNAL	257	FT	DISULFID	248	257	BY SIMILARITY.
FT	CHAIN	264	FT	DISULFID	264	275	BY SIMILARITY.
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FT	CHAIN	2471	FT	DISULFID	1372	1383	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1383	1394	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1394	1405	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1405	1416	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1416	1427	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1427	1438	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1438	1449	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1449	1460	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1460	1471	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1471	1482	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1482	1493	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1493	1504	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1504	1515	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1515	1526	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1526	1537	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1537	1548	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1548	1559	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1559	1570	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1570	1581	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1581	1592	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1592	1603	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1603	1614	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1614	1625	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1625	1636	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1636	1647	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1647	1658	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1658	1669	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1669	1680	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1680	1691	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1691	1702	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1702	1713	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1713	1724	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1724	1735	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1735	1746	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1746	1757	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1757	1768	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1768	1779	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1779	1790	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1790	1801	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1801	1812	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1812	1823	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1823	1834	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1834	1845	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1845	1856	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1856	1867	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1867	1878	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1878	1889	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1889	1900	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1900	1911	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1911	1922	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1922	1933	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1933	1944	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1944	1955	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1955	1966	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1966	1977	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1977	1988	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1988	1999	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	1999	2010	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	2010	2021	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	2021	2032	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	2032	2043	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	2043	2054	BY SIMILARITY.
FT	CHAIN	2471	FT	DISULFID	2054	2065	BY SIMILARITY.
FT	CHAIN	2					



Db 1008 SerPheSer-CysLeuCysProValGlyPheThrGlyPro 1020

RESULT 3

NTC3\_MOUSE

ID NTC3\_MOUSE STANDARD; PRT; 2318 AA.

AC Q61982;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neurogenic locus notch homolog protein 3 precursor (Notch 3).

GN NOTCH3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ICR X Swiss Webster;

RA MEDLINE=95001556; PubMed=7918037;

RA Lardelli M., Dalstrand J., Lendahl U.;

RT "The novel Notch homologue mouse Notch 3 lacks specific epidermal

RT growth factor-repeats and is expressed in proliferating

RT neuroepithelium.";

RL Mech. Dev. 46:123-136(1994).

RN [2]

RP POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1664.

RX MEDLINE=21523956; PubMed=11518718;

RA Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;

RT "Murine notch homologs (NL-4) undergo presenilin-dependent

RT proteolysis.";

RL J. Biol. Chem. 276:40268-40273(2001).

RN [3]

RP POST-TRANSLATIONAL PROCESSING.

RX MEDLINE=21374376; PubMed=1145941;

RA Mizutani T., Taniuchi Y., Aoki T., Hashimoto N., Honjo T.;

RT "Conservation of the biochemical mechanisms of signal transduction

RT among mammalian Notch family members.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).

CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands

CC Jagged1, Jagged2 and Delta to regulate cell-fate determination.

CC Upon ligand activation through the released notch intracellular

CC domain (NICD) it forms a transcriptional activator complex with

CC RBP-J kappa and activates genes of the enhancer of split locus.

CC Affects the implementation of differentiation, proliferation and

CC apoptotic programs (By similarity). May play a role during CNS

CC development.

CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TW) and a N-

CC terminal fragment N(EC) which are probably linked by disulfide

CC bonds.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following

CC proteolytical processing NICD is translocated to the nucleus.

CC -!- TISSUE SPECIFICITY: Proliferating neuroepithelium.

CC -!- DEVELOPMENTAL STAGE: CNS development.

CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form

CC which is proteolytically cleaved by a furin-like convertase in the

CC trans-Golgi network before it reaches the plasma membrane to yield

CC an active, ligand-accessible form. Cleavage results in a C-

CC terminal fragment N(TW) and a N-terminal fragment N(EC). Following

CC ligand binding, it is cleaved by TNF-alpha converting enzyme

CC (TACE) to yield a membrane-associated intermediate fragment called

CC notch extracellular truncation (NEXT). This fragment is then

CC cleaved by presenilin dependent gamma-secretase to release a

CC notch-derived peptide containing the intracellular domain (NICD)

CC from the membrane.

CC -!- PTM: Phosphorylated.

CC -!- SIMILARITY: Belongs to the NOTCH family.

CC -!- SIMILARITY: Contains 34 EGF-like domains.

CC -!- SIMILARITY: Contains 3 lin/Notch repeats.

CC -!- SIMILARITY: Contains 5 ANK repeats.

CC

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

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CC EMBL; X74760; CAA52776.1; --

CC PIR; S45306; S45306.

CC HSP; P00740; IEDM.

CC MGD; MGI-99460; Notch3.

CC GO; GO:0005887; C:integral to plasma membrane; IC.

CC GO; GO:0005915; F:protein binding; IPI.

CC GO; GO:0007219; P:N signaling pathway; IC.

CC GO; GO:0007219; P:N signaling pathway; IC.

CC InterPro; IPR002110; ANK.

CC InterPro; IPR000152; Asx hydroxyl\_s.

CC InterPro; IPR000742; EGF\_2.

CC InterPro; IPR001881; EGF\_Ca.

CC InterPro; IPR001438; EGF\_II.

CC InterPro; IPR006209; EGF\_Like.

CC InterPro; IPR002049; Laminin\_EGF.

CC InterPro; IPR008297; Notch.

CC InterPro; IPR000800; Notch\_dom.

CC Pfam; PF00023; ank; 6.

CC Pfam; PF00008; EGF; 33.

CC Pfam; PF00066; Notch; 3.

CC PIRSF; PIRSF002279; Notch; 1.

CC PRINTS; PR00010; EGFBL00D.

CC PRINTS; PR00011; EGF\_LAMININ.

CC PRINTS; PR01452; NOTCH.

CC SMART; SM00248; ANK; 6.

CC SMART; SW00179; EGF\_Ca; 19.

CC SMART; SW00004; NL; 3.

CC PROSITE; PS00297; ANK\_REPEAT\_REGION; 1.

CC PROSITE; PS00088; ANK\_REPEAT; 4.

CC PROSITE; PS00010; ASX\_HYDROXYL; 18.

CC PROSITE; PS00022; EGF\_1; 33.

CC PROSITE; PS01186; EGF\_2; 27.

CC PROSITE; PS00026; EGF\_3; 34.

CC PROSITE; PS01187; EGF\_Ca; 16.

CC Receptor; Transcription regulation; Activator; Differentiation;

CC Developmental protein; Repeat; ANK repeat; EGF-like domain;

CC Transmembrane; Glycoprotein; Signal; Phosphorylation.

CC SIGNAL 1 39

CC CHAIN 40 2318 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 3.

CC CHAIN 1630 2318 NOTCH EXTRACELLULAR TRUNCATION.

CC CHAIN 1863 2318 NOTCH INTRACELLULAR DOMAIN.

CC DOMAIN 40 1643 EXTRACELLULAR.

CC TRANSMEM 1644 1664 POTENTIAL.

CC DOMAIN 1665 2318 CYTOPLASMIC.

CC DOMAIN 2242 2261 PEST.

CC DOMAIN 40 78 EGF-LIKE 1.

CC DOMAIN 79 119 EGF-LIKE 2.

CC DOMAIN 120 157 EGF-LIKE 3.

CC DOMAIN 159 196 EGF-LIKE 4. CALCIUM-BINDING (POTENTIAL).

CC DOMAIN 198 235 EGF-LIKE 5.

CC DOMAIN 237 273 EGF-LIKE 6. CALCIUM-BINDING (POTENTIAL).

CC DOMAIN 275 313 EGF-LIKE 7.

CC DOMAIN 315 351 EGF-LIKE 8. CALCIUM-BINDING (POTENTIAL).

CC DOMAIN 352 390 EGF-LIKE 9.

CC DOMAIN 392 430 EGF-LIKE 10. CALCIUM-BINDING (POTENTIAL).

CC DOMAIN 432 468 EGF-LIKE 11. CALCIUM-BINDING (POTENTIAL).

CC DOMAIN 470 506 EGF-LIKE 12. CALCIUM-BINDING (POTENTIAL).

CC DOMAIN 508 544 EGF-LIKE 13. CALCIUM-BINDING (POTENTIAL).

CC DOMAIN 546 581 EGF-LIKE 14. CALCIUM-BINDING (POTENTIAL).

CC DOMAIN 583 619 EGF-LIKE 15. CALCIUM-BINDING (POTENTIAL).

CC DOMAIN 621 656 EGF-LIKE 16. CALCIUM-BINDING (POTENTIAL).

CC DOMAIN 658 694 EGF-LIKE 17. CALCIUM-BINDING (POTENTIAL).

CC DOMAIN 696 731 EGF-LIKE 18.

CC DOMAIN 735 771 EGF-LIKE 19.

CC DOMAIN 772 809 EGF-LIKE 20.

CC DOMAIN 811 848 EGF-LIKE 21. CALCIUM-BINDING (POTENTIAL).

CC DOMAIN 850 886 EGF-LIKE 22. CALCIUM-BINDING (POTENTIAL).

CC DOMAIN 888 923 EGF-LIKE 23. CALCIUM-BINDING (POTENTIAL).

CC DOMAIN 925 961 EGF-LIKE 24.

FT	DOMAIN	963	999	EGF-LIKE 25.	
FT	DOMAIN	1001	1035	EGF-LIKE 26.	
FT	DOMAIN	1037	1083	EGF-LIKE 27.	
FT	DOMAIN	1085	1121	EGF-LIKE 28.	
FT	DOMAIN	1123	1159	EGF-LIKE 29.	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	1161	1204	EGF-LIKE 30.	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	1206	1245	EGF-LIKE 31.	
FT	DOMAIN	1247	1288	EGF-LIKE 32.	
FT	DOMAIN	1290	1326	EGF-LIKE 33.	
FT	DOMAIN	1336	1374	EGF-LIKE 34.	
FT	REPEAT	1388	1428	LIN/NOTCH 1.	
FT	REPEAT	1429	1467	LIN/NOTCH 2.	
FT	REPEAT	1468	1503	LIN/NOTCH 3.	
FT	REPEAT	1839	1868	ANK 1.	
FT	REPEAT	1872	1902	ANK 2.	
FT	REPEAT	1906	1935	ANK 3.	
FT	REPEAT	1939	1968	ANK 4.	
FT	REPEAT	1972	2001	ANK 5.	
FT	SITE	1572	1573	CLEAVAGE (BY FURIN-LIKE PROTEASE) (BY SIMILARITY).	
FT	DISULFID	43	55	BY SIMILARITY.	
FT	DISULFID	49	66	BY SIMILARITY.	
FT	DISULFID	68	77	BY SIMILARITY.	
FT	DISULFID	83	94	BY SIMILARITY.	
FT	DISULFID	88	107	BY SIMILARITY.	
FT	DISULFID	109	118	BY SIMILARITY.	
FT	DISULFID	124	135	BY SIMILARITY.	
FT	DISULFID	129	145	BY SIMILARITY.	
FT	DISULFID	147	156	BY SIMILARITY.	
FT	DISULFID	163	175	BY SIMILARITY.	
FT	DISULFID	169	184	BY SIMILARITY.	
FT	DISULFID	186	195	BY SIMILARITY.	
FT	DISULFID	202	213	BY SIMILARITY.	
FT	DISULFID	207	223	BY SIMILARITY.	
FT	DISULFID	225	234	BY SIMILARITY.	
FT	DISULFID	241	252	BY SIMILARITY.	
FT	DISULFID	246	261	BY SIMILARITY.	
FT	DISULFID	263	272	BY SIMILARITY.	
FT	DISULFID	279	292	BY SIMILARITY.	
FT	DISULFID	286	301	BY SIMILARITY.	
FT	DISULFID	303	312	BY SIMILARITY.	
FT	DISULFID	319	330	BY SIMILARITY.	
FT	DISULFID	324	339	BY SIMILARITY.	
FT	DISULFID	341	350	BY SIMILARITY.	
FT	DISULFID	356	367	BY SIMILARITY.	
FT	DISULFID	361	378	BY SIMILARITY.	
FT	DISULFID	380	389	BY SIMILARITY.	
FT	DISULFID	396	409	BY SIMILARITY.	
FT	DISULFID	403	418	BY SIMILARITY.	
FT	DISULFID	420	429	BY SIMILARITY.	
FT	DISULFID	436	447	BY SIMILARITY.	
FT	DISULFID	441	456	BY SIMILARITY.	
FT	DISULFID	458	467	BY SIMILARITY.	
FT	DISULFID	474	485	BY SIMILARITY.	
FT	DISULFID	479	494	BY SIMILARITY.	
FT	DISULFID	496	505	BY SIMILARITY.	
FT	DISULFID	512	523	BY SIMILARITY.	
FT	DISULFID	517	532	BY SIMILARITY.	
Alignment Scores:					
Pred. No.:		0.0135	Length:	2318	
Score:		103.00	Matches:	28	
Percent Similarity:		40.62%	Conservative:	11	
Best Local Similarity:		29.17%	Mismatches:	21	
Query Match:		11.60%	Indels:	36	
DB:		1	Gaps:	6	
US-09-773-476-294 (1-489) x NTC3_MOUSE (1-2318)					
Qy	140	CTCAGACTCTGATCTACACAGATGTTCCCTGT	-----	175	
Db	689	LeuProProLeuCysLeuProAlaAsnHisProCysAlaHisLysProCysSerHisGly	-----	708	

Qy	176	-----CCTGGAGGTAGTAATGCTGGACAACTGTTACTTCTTCAAGGAC	220
Db	709	ValCysHisAspAlaProGlyGlyPheArgCys-----	719
Qy	221	AGCAGATTTCCTCAA-----GGCAAGGACCTTTGCAATAGCACTGGAAGC	268
Db	720	-----ValCysGluProGlyTrpSerGlyProArg-----CysSerGlnSerLeuAla	735
Qy	269	CCAGAAATGTCCTCTGAG-----AACGGATCTTGTGCATCTGACGGTCTCT	313
Db	736	ProAspAlaCysGluSerGlnProCysGlnAlaGlyGlyThrCysThrSerAspGlyIle	755
Qy	314	GGTCTTTTGCAGTCGCTTGTGCTGATGGTTCCATGGATACAAAGTGT	361
Db	756	Gly-----PheArgCysThrCysAlaProGlyPheGlnGlyHisGlnCys	770
RESULT 4			
ID	NTC1_MOUSE	STANDARD;	PRT; 2531 AA.
AC	Q01705; Q06007; Q61905; Q99JC2; Q9QM58; Q9R0X7;		
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-FEB-1996 (Rel. 33, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Neurogenic locus notch homolog protein 1 precursor (Notch 1) (Notch A)		
DE	(MT14) (p300).		
GN	NOTCH1 OR NOTCH.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
[1]	SEQUENCE FROM N.A. (ISOFORM 1).		
RP	TISSUE=Embryo;		
RC	MEDLINE=93194170; PubMed=8449489;		
RX	Franco del Amo F., Gendron-Maguire M., Swiatek P.J., Jenkins N.A.,		
RA	Copeland N.G., Gridley T.;		
RT	"Cloning, analysis, and chromosomal localization of Notch-1, a mouse		
RT	homolog of Drosophila Notch.;"		
RL	Genomics 15:259-264(1993).		
[2]	SEQUENCE OF 731-1899 FROM N.A. (ISOFORM 2), AND DEVELOPMENTAL STAGE.		
RP	STRAIN=CD-1; TISSUE=Embryo;		
RC	MEDLINE=93050801; PubMed=1426644;		
RX	Reaume A.G., Conlon R.A., Zirngibl R., Yamaguchi T.P., Rossant J.;		
RA	"Expression analysis of a Notch homologue in the mouse embryo.;"		
RT	Dev. Biol. 154:377-387(1992).		
RL	[3]		
RP	SEQUENCE OF 1551-1647 FROM N.A. (ISOFORM 1), AND DEVELOPMENTAL STAGE.		
RC	TISSUE=Embryo;		
RX	MEDLINE=93048835; PubMed=1425352;		
RA	Franco del Amo F., Smith D.E., Swiatek P.J., Gendron-Maguire M.,		
RA	Greenspan R.J., McMahon A.P., Gridley T.;		
RT	"Expression pattern of Notch, a mouse homolog of Drosophila Notch,		
RT	suggests an important role in early postimplantation mouse		
RT	development.;"		
RL	Development 115:737-744(1992).		
RN	[4]		
RP	SEQUENCE OF 1161-1547 FROM N.A.		
RC	STRAIN=C57BL/6 X CBA; TISSUE=Embryo;		
RX	MEDLINE=93178563; PubMed=8440332;		
RA	Lardelli M., Lendahl U.;		
RT	"Notch A and Notch B-two mouse Notch homologues coexpressed in a		
RT	wide variety of tissues.;"		
RL	Exp. Cell Res. 204:364-372(1993).		
RN	[5]		
RP	SEQUENCE OF 1659-1673 FROM N.A.		
RX	MEDLINE=93164499; PubMed=10437788;		
RA	Lee J.S., Ishimoto A., Yanagawa S.I.;		
RT	"Murine leukemia provirus-mediated activation of the Notch1 gene leads		
RT	to induction of HES-1 in a mouse T lymphoma cell line, DU-3.;"		
RL	FEBS Lett. 455:276-280(1999).		
RN	[6]		
RP	SEQUENCE OF 1950-2201 FROM N.A.		

MEDLINE=98029496; PubMed=9384671;  
RA Messerie M., Folio M., Nehls M., Eggert H., Boehm T.;  
RT "Dynamic changes in gene expression during in vitro differentiation of  
RL mouse embryonic stem cells";  
RN Cytokines Cell. Mol. Ther. 1:139-143(1995).  
[7]  
RP SEQUENCE OF 1555-1659, CLEAVAGE BY FURIN-LIKE CONVERTASE, AND  
RP MUTAGENESIS OF 1651-ARG--ARG-1654.  
RX MEDLINE=98318619; PubMed=9653148;  
RA Logeat F., Bessia C., Brou C., LeBail O., Jarriault S., Seidah N.G.,  
RA Israel A.;  
RT "The Notch1 receptor is cleaved constitutively by a furin-like  
RL convertase";  
RN Proc. Natl. Acad. Sci. U.S.A. 95:8108-8112(1998).  
[8]  
RP PARTIAL SEQUENCE, AND POST-TRANSLATIONAL PROCESSING.  
RP MEDLINE=21523956; PubMed=11518718;  
RX Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;  
RA "Murine notch homologs (N1-4) undergo presenilin-dependent  
RL proteolysis";  
RN J. Biol. Chem. 276:40268-40273(2001).  
[9]  
RP POST-TRANSLATIONAL PROCESSING.  
RP MEDLINE=21374376; PubMed=11459941;  
RX Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;  
RA "Conservation of the biochemical mechanisms of signal transduction  
RL among mammalian Notch family members";  
RN Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).  
[10]  
RP INTERACTION WITH DTX1 AND DTX2.  
RP MEDLINE=21123790; PubMed=11226752;  
RX Kishi N., Tang Z., Maeda Y., Hirai A., Mo R., Ito M., Suzuki S.,  
RA Nakao K., Kinoshita T., Kadesch T., Hui C.-C., Attavanis-Teakonas S.,  
RA Okano H., Matsuno K.;  
RT "Murine homologs of deltex define a novel gene family involved in  
RL vertebrate Notch signaling and neurogenesis.";  
RN Int. J. Dev. Neurosci. 19:21-35(2001).  
-!- FUNCTION: Functions as a receptor for membrane-bound ligands  
CC Jagged1, Jagged2 and Delta to regulate cell-fate determination.  
CC Upon ligand activation through the released notch intracellular  
CC domain (NICD) it forms a transcriptional activator complex with  
CC RBP-J kappa and activates genes of the enhancer of split locus.  
CC Affects the implementation of differentiation, proliferation and  
CC apoptotic programs (by similarity). May play an essential role in  
CC postimplantation development, probably in some aspect of cell  
CC specification and/or differentiation. May be involved in mesoderm  
CC development, somite formation and neurogenesis. Involved in the  
CC maturation of both CD4+ and CD8+ cells in the thymus.  
CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-  
CC terminal fragment N(IEC) which are probably linked by disulfide  
CC bonds. Interacts with DTX1 and DTX2.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following  
CC proteolytical processing NICD is translocated to the nucleus.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q01705-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q01705-2; Sequence=VSP\_001402, VSP\_001403, VSP\_001404;  
CC Note=No experimental confirmation available;  
CC -!- TISSUE SPECIFICITY: Highly expressed in the brain, lung and  
CC thymus. Expressed at lower levels in the spleen, bone-marrow,  
CC spinal cord, eyes, mammary gland, liver, intestine, skeletal  
CC muscle, kidney and heart.  
CC -!- DEVELOPMENTAL STAGE: First detected in the mesoderm at 7.5 dpc By  
CC 8.5 dpc highly expressed in presomitic mesoderm, mesenchyme and  
CC endothelial cells, while much lower levels are seen in the  
CC neuroepithelium. Between 9.5-10.5 dpc expressed at high levels in  
CC the neuroepithelium. At 13.5 dpc expressed in the surface  
CC ectoderm, eye and developing whisker follicles.  
CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form  
CC which is proteolytically cleaved by a furin-like convertase in the  
CC trans-Golgi network before it reaches the plasma membrane to yield

an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presenilin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane.

-1- PTM: Phosphorylated.  
CC  
CC -1- SIMILARITY: Belongs to the NOTCH family.  
CC  
CC -1- SIMILARITY: Contains 36 EGF-like domains.  
CC  
CC -1- SIMILARITY: Contains 3 Lin/Notch repeats.  
CC  
CC -1- SIMILARITY: Contains 5 ANK repeats.  
CC

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CC

EMBL; Z11886; CAA77941.1; -;  
DR ENBL; L02613; AAK14898.1; -;  
CC ENBL; X68278; CAA48339.1; -;  
DR ENBL; AJ238029; CAB40733.1; -;  
CC ENBL; X82562; CAA57909.1; -;  
DR PIR; A46019; A46019.  
CC PIR; B49175; B49175.  
DR HSPR; P00740; IEDM.  
CC MGSD; MGI:97363; Notchl.  
DR GO; GO:0005887; Cr: integral to plasma membrane; IC.  
CC GO; GO:0005515; F: protein binding; IPI.  
DR GO; GO:0003054; P: cell differentiation; IMP.  
CC GO; GO:0007386; P: compartment specification; IMP.  
DR GO; GO:0007219; P: n signaling pathway; IC.  
CC GO; GO:0045344; P: positive regulation of transcription from p...; IDA.  
DR InterPro; IPR002110; ANK.  
CC InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR000742; EGF\_2.  
CC InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001438; EGF\_II.  
CC InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR002049; Laminin\_EGF.  
CC InterPro; IPR008297; Notch.  
DR InterPro; IPR000800; Notch\_dom.  
CC Pfam; PF000023; ank; 7.  
DR Pfam; PF00008; EGF; 35.  
CC Pfam; PF00066; notch; 3.  
DR PIRSF; PIRSF002279; Notch; 1.  
CC PRINTS; PR00010; EGFBLOOD.  
DR PRINTS; PR00011; EGF\_LAMININ.  
CC PRINTS; PR01452; NOTCH.  
DR SMART; SMO0248; ANK; 6.  
CC SMART; SMO0179; EGF\_CA; 24.  
DR SMART; SMO0004; NL; 2.  
CC PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
DR PROSITE; PS50088; ANK\_REPEAT; 2.  
CC PROSITE; PS00010; ASX\_HYDROXYL; 22.  
DR PROSITE; PS00023; EGF\_1; 34.  
CC PROSITE; PS01186; EGF\_2; 27.  
DR PROSITE; PS50026; EGF\_3; 36.  
CC PROSITE; PS01187; EGF\_CA; 21.  
DR Kwd Receptor; Transcription regulation; Activator; Differentiation;  
KW Developmental protein; Repeat; ANK repeat; EGF-like domain;  
KM Transmembrane; Glycoprotein; Signal; Phosphorylation;  
KW Alternative splicing; 18  
CC SIGNAL 1  
FT CHAIN 19 2531 POTENTIAL.  
FT CHAIN 1711 2531 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1.  
FT CHAIN 1744 2531 NOTCH EXTRACELLULAR TRUNCATION.  
FT CHAIN 19 1725 NOTCH INTRACELLULAR DOMAIN.  
FT DOMAIN 19 1725 EXTRACELLULAR (POTENTIAL).

[illegible]

Alignment Scores: 0.0137 Length: 2531  
 Pred. No.: 103.00 Matches: 41  
 Score: 103.00  
 Percent Similarity: 35.80% Conservative: 17  
 Best Local Similarity: 25.31% Mismatches: 53  
 Query Match: 11.60% Indels: 51  
 DB: 1 Gaps: 8

US-09-773-476-294 (1-489) x NTC1\_MOUSE (1-2531)

QY 53 TTACAGGCTTATCT-----GCTATTATCATAGACCTTCAG-----GGAATTCCT 97  
 Db 441 LeuGlnGlyThrGlyProGlyCysGluLeuPheGlnGlyCysLeuSerAsnPro 460  
 QY 98 CTCAGAGATGTTGGCAACACCTTCGGTGGTTCCTACTCAGTCGACGCTCTGATCTA 157  
 Db 461 CysGlnAsnAsp---AlaThrCysLeuAspGlnIleGlyGluPheGlnCysIleCysMet 479  
 QY 158 CCA-----CAAGATGTTCCCTGT 175  
 Db 480 ProGlyTyrgluGlyValTyrcysGluLeuAsnThrAspGluCysAlaSerSerProCys 499  
 QY 176 CCTGGAGTGTATGCTGGCAACATGTTACTTCTTTTCAAG----- 217  
 Db 500 LeuHisAsnGlyHisCysMetAspLysIleHisGluPheGlnCysGlnCysProLysGly 519  
 QY 218 ---CACAGCAGATTGCCAGGCAAGGACCTTTCGATAGCAGCTGGAAGCCAGAA 274  
 Db 520 PheAsnGlyHisLeuCysGlnTyrcysValAspGluCysAlaSerThr----- 535  
 QY 275 ATGTGCTCTCAGACGAGATCTTGTGCATCTCAGCGTCTCTGCTTTTGCAGTCCGTTGT 334  
 Db 536 ProCys---LysAsnGlyAlaLysCysLeuAspGlyProAsnThrTyrcysValCys 554  
 QY 335 GCTCATGTTCCATGATACAGTGT----- 361  
 Db 555 ThrGluGlyTyrcysGlyHisCysGluValAspGluCysAspProAspPro 574  
 QY 362 -----ATGAGCAGGCTCATTTTCACTGCTTATGTTCTTTGGG 400  
 Db 575 CysHisTyrglySerCysLysAsp-GlyValAlaThrPheThrCysLeuCysGlnProGln 594  
 QY 401 ATTC 404  
 Db 594 yTyr 595

RESULT 5  
 NTC2\_HUMAN  
 ID NTC2\_HUMAN STANDARD; PRT; 2471 AA.  
 AC Q04721; Q99734; Q9H240;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Neurogenic locus notch homolog protein 2 precursor (Notch 2) (hN2).  
 GN NOTCH2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Blaumüller C.M., Mann R.S.;  
 RT "Complete human notch 2 (hN2) cDNA sequence.";  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Breast tumor;  
 RA Correa R.G., Camargo A.A., Moreira E.S., Simpson A.J.G.;  
 RT "Human Notch2, a novel member of cell-fate determining NOTCH family.";  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]

SEQUENCE OF 967-1229 FROM N.A.  
 TISSUE=T-cell;  
 Lemasson I., Devaux C., Mesnard J.M.;  
 "Partial sequence of EGF-like repeat domain of human Notch2 mRNA.";  
 Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 (4)  
 SEQUENCE OF 1810-2447 FROM N.A.  
 TISSUE=Brain;  
 MEDLINE=93265135; PubMed=1303260;  
 Stifani S., Blaumüller C.M., Redhead N.J., Hall R.E.,  
 Artavanis-Tsakonas S.;  
 "Human homologs of a Drosophila enhancer of split gene product define a novel family of nuclear proteins.";  
 Nat. Genet. 2:119-127(1992).  
 (5)  
 POST-TRANSLATIONAL PROCESSING.  
 MEDLINE=97386453; PubMed=9244302;  
 Blaumüller C.M., Qi H., Zagouras P., Artavanis-Tsakonas S.;  
 "Intracellular cleavage of Notch leads to a heterodimeric receptor on the plasma membrane.";  
 Cell 90:281-291(1997).  
 (6)  
 IDENTIFICATION OF LIGANDS.  
 MEDLINE=99180765; PubMed=10079256;  
 Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L., Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;  
 "Human ligands of the Notch receptor.";  
 Am. J. Pathol. 154:785-794(1999).  
 CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands Jagged1, Jagged2 and Delta to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity).  
 CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide bonds (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus.  
 CC -!- TISSUE SPECIFICITY: Expressed in the brain, heart, kidney, lung, skeletal muscle and liver.  
 CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presenilin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane (By similarity).  
 CC -!- PTM: Phosphorylated (By similarity).  
 CC -!- SIMILARITY: Belongs to the NOTCH family.  
 CC -!- SIMILARITY: Contains 35 EGF-like domains.  
 CC -!- SIMILARITY: Contains 2 Lin/Notch repeats.  
 CC -!- SIMILARITY: Contains 6 ANK repeats.  
 CC -----  
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 CC -----  
 CC EMBL; AF308601; AA36377.2; -;  
 CC EMBL; AF353566; AAG37073.1; -;  
 CC EMBL; U77493; AAB19224.1; -;  
 CC HSSP; P00740; 1EDM.  
 CC Genew; HGNC:7882; NOTCH2.  
 CC MIM; 600275; -;

DR InterPro: IPR002110; ANK.  
 DR InterPro: IPR000152; Asx\_hydroxyl\_S.  
 DR InterPro: IPR000742; EGF\_2.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR001438; EGF\_II.  
 DR InterPro: IPR006209; EGF-like.  
 DR InterPro: IPR002049; Laminin\_EGF.  
 DR InterPro: IPR008237; Notch.  
 DR InterPro: IPR000800; Notch\_dom.  
 DR Pfam: PF00023; ank; 6.  
 DR Pfam: PF00008; EGF; 35.  
 DR Pfam: PF00066; notch; 2.  
 DR PIRSF: PIRSF002279; Notch; 1.  
 DR PRINTS: PRO0010; EGFBL00D.  
 DR PRINTS: PRO0011; EGF\_LAMININ.  
 DR PRINTS: PRO1452; NOTCH.  
 DR SMART: SM00248; ANK; 6.  
 DR SMART: SM00179; EGF\_Ca; 23.  
 DR SMART: SM00004; NL; 2.  
 DR PROSITE: PS00297; ANK REP REGION; 1.  
 DR PROSITE: PS00088; ANK REPEAT; 4.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 22.  
 DR PROSITE: PS00022; EGF\_1; 34.  
 DR PROSITE: PS01186; EGF\_2; 29.  
 DR PROSITE: PS00026; EGF\_3; 35.  
 DR PROSITE: PS01187; EGF\_Ca; 22.  
 KW Receptor; Transcription regulation; Activator; Differentiation;  
 KW Developmental protein; Repeat; ANK repeat; EGF-like domain;  
 KW Transmembrane; Glycoprotein; Signal; Phosphorylation.  
 FT SIGNAL 1 25  
 FT CHAIN 26 2471  
 FT CHAIN 1666 2471  
 FT CHAIN 1697 2471  
 FT DOMAIN 26 1677  
 FT TRANSMEM 1678 1698  
 FT DOMAIN 1699 2471  
 FT DOMAIN 26 63  
 FT DOMAIN 64 102  
 FT DOMAIN 105 143  
 FT DOMAIN 144 180  
 FT DOMAIN 182 219  
 FT DOMAIN 221 258  
 FT DOMAIN 260 296  
 FT DOMAIN 298 336  
 FT DOMAIN 338 374  
 FT DOMAIN 375 413  
 FT DOMAIN 415 454  
 FT DOMAIN 456 492  
 FT DOMAIN 494 530  
 FT DOMAIN 532 568  
 FT DOMAIN 570 605  
 FT DOMAIN 607 643  
 FT DOMAIN 645 680  
 FT DOMAIN 682 718  
 FT DOMAIN 720 755  
 FT DOMAIN 757 793  
 FT DOMAIN 795 831  
 FT DOMAIN 833 871  
 FT DOMAIN 873 909  
 FT DOMAIN 911 947  
 FT DOMAIN 949 985  
 FT DOMAIN 987 1023  
 FT DOMAIN 1025 1061  
 FT DOMAIN 1063 1099  
 FT DOMAIN 1101 1147  
 FT DOMAIN 1149 1185  
 FT DOMAIN 1187 1223  
 FT DOMAIN 1225 1262  
 FT DOMAIN 1264 1302  
 FT DOMAIN 1304 1343  
 FT DOMAIN 1374 1412

FT REPEAT 1420 1456 LIN/NOTCH 1.  
 FT REPEAT 1503 1535 LIN/NOTCH 2.  
 FT REPEAT 1827 1871 ANK 1.  
 FT REPEAT 1876 1905 ANK 2.  
 FT REPEAT 1909 1939 ANK 3.  
 FT REPEAT 1943 1972 ANK 4.  
 FT REPEAT 1976 2005 ANK 5.  
 FT REPEAT 2009 2038 ANK 6.  
 FT DOMAIN 1645 1648 POLY-ALA.  
 FT DOMAIN 1994 1997 POLY-LEU.  
 FT DOMAIN 2426 2429 POLY-SER.  
 FT DISULFID 28 41 BY SIMILARITY.  
 FT DISULFID 35 51 BY SIMILARITY.  
 FT DISULFID 53 62 BY SIMILARITY.  
 FT DISULFID 68 79 BY SIMILARITY.  
 FT DISULFID 73 90 BY SIMILARITY.  
 FT DISULFID 92 101 BY SIMILARITY.  
 FT DISULFID 109 121 BY SIMILARITY.  
 FT DISULFID 115 131 BY SIMILARITY.  
 FT DISULFID 133 142 BY SIMILARITY.  
 FT DISULFID 148 159 BY SIMILARITY.  
 FT DISULFID 153 168 BY SIMILARITY.  
 FT DISULFID 170 179 BY SIMILARITY.  
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 FT DISULFID 192 207 BY SIMILARITY.  
 FT DISULFID 209 218 BY SIMILARITY.  
 FT DISULFID 225 236 BY SIMILARITY.  
 FT DISULFID 230 246 BY SIMILARITY.  
 FT DISULFID 248 257 BY SIMILARITY.  
 Alignment Scores:  
 Pred. No.: 0.0174 Length: 2471  
 Score: 102.00 Matches: 42  
 Percent Similarity: 36.18% Conservative: 13  
 Best Local Similarity: 27.63% Mismatches: 48  
 Query Match: 11.49% Indels: 49  
 DB: 1 Gaps: 8  
 US-09-773-476-294 (1-489) x NTC2\_HUMAN (1-2471)  
 QY 74 ATCATAGACCTTCAGGCAAAATCTCTCAAGAT-----GATTTGGCCAAAC 118  
 DB 912 ILeAspSerCysLeuAlaAsnProCysGlnAsnGlyGlySerCysMetAspGlyValAsn 931  
 QY 119 ACCTTCGGT-----GGTTTACT-----CAGCTGCAGACTCTGATACTA 157  
 DB 932 ThrPheSerCysLeuCysLeuProGlyPheThrGlyAspLysCysGlnThr----- 948  
 QY 158 CCACAAGATGT-----CCCTGTCTGGAGTACTAATGCCTGGGAC 199  
 DB 949 -----AspMetAsnGluCysLeuSerGluProCysLysAsnGlyGlyThrCysSerAsp 966  
 QY 200 AATGTTACTTTTCAAGGACAAGCAGATTGGCAAGGGCAAGGGACCTTTGCAATAGC 259  
 DB 967 TyrValAsnSerTyrThrCysLys-----CysGlnAlaGlyPheAspGlyValHisCys 984  
 QY 260 ACTGGAGGCCAGAAATGTCTCTGAG-----AACGATCTTGTGCATCTGAC 307  
 DB 985 GluAsnAsnLeuAsnGluCysThrGluSerSerCysPheAsnGlyGlyThrCysValAsp 1004  
 QY 308 GGTCTGTCTTTTGCAGTGGTTTGTGTCATGCTTCCATGATGATGATGATGAGG 367  
 DB 1005 GlyIleAsnSerPheSerCysLeuCysProValGlyPheThrGlySerPheCysLeuHis 1024  
 QY 368 CAG----- 370  
 DB 1025 GluIleAsnGluCysSerSerHisProCysLeuAsnGluGlyThrCysValAspGlyLeu 1044  
 QY 371 GGCTCATTTTCACGTCTTATGTTCTTTGGGATTC 404  
 DB 1045 GlyThr-TyrArgCysSerCysProLeuGlyTyr 1055

RESULT 6

NOTC DROME STANDARD; PRT: 2703 AA.  
 ID P07207; 097458; P04154; Q9W4T8;  
 AC 01-NOV-1986 (Rel. 03, Created)  
 DT 28-FEB-2003 (Rel. 43, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Neurogenic locus Notch protein precursor.  
 GN N OR EG:140611.1 OR EG:163A10.2 OR CG3936.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NEB1\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Oregon-R; TISSUE=Embryo;  
 RX MEDLINE=86079539; PubMed=3935325;  
 RA Wharton K.A., Johansen K.M., Xu T., Artavanis-Tsakonas S.;  
 RT "Nucleotide sequence from the neurogenic locus notch implies a gene  
 RT product that shares homology with proteins containing EGF-like  
 RT repeats.";  
 RL Cell 43:567-581 (1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Canton-S, and Oregon-R; TISSUE=Embryo;  
 RX MEDLINE=97064624; PubMed=3097517;  
 RA Kidd S., Kelley M.R., Young M.W.;  
 RT "Sequence of the notch locus of Drosophila melanogaster: relationship  
 RT of the encoded protein to mammalian clotting and growth factors.";  
 RL Mol. Cell. Biol. 6:3094-3108 (1986).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=20196005; PubMed=10731132;  
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA April J.P., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,  
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hestlin D., Houston K.A., Howland T.J., Wei M.-H., thegwan C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M., M.G.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195 (2000).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Oregon-R;  
 RX MEDLINE=10731137;  
 RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,  
 RA Barrell B.G., Ferraz C., Vidal S., Brun C., Denailles J., Cadieu E.,  
 RA Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,  
 RA Minano B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,  
 RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,  
 RA Mcdolell J., Peter A., Schoettler P., Werner M., Mourikioti F.,  
 RA Beinert N., Dowe G., Schaefer U., Jaackle H., Bucheton A.,  
 RA Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,  
 RA McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,  
 RA Glover D.M.;  
 RT "From sequence to chromosome: the tip of the X chromosome of D.  
 RT melanogaster.";  
 RL Science 287:2220-2222 (2000).  
 RN [5]  
 RP SEQUENCE OF 2505-2611 FROM N.A.  
 RX MEDLINE=85093929; PubMed=2981631;  
 RA Wharton K.A., Yedvobnick B., Finnerty V.G., Artavanis-Tsakonas S.;  
 RT "opa: a novel family of transcribed repeats shared by the Notch locus  
 RT and other developmentally regulated loci in D. melanogaster.";  
 RL Cell 40:55-62 (1985).  
 RN [6]  
 RP SEQUENCE OF 1-8 FROM N.A.  
 RX MEDLINE=87257846; PubMed=3037327;  
 RA Kelley M.R., Kidd S., Berg R.L., Young M.W.;  
 RT "Restriction of P-element insertions at the Notch locus of Drosophila  
 RT melanogaster.";  
 RL Mol. Cell. Biol. 7:1545-1548 (1987).  
 RN [7]  
 RP INTERACTION WITH DX. AND MUTANT SU42C.  
 RX MEDLINE=94215489; PubMed=8162948;  
 RA Diederich R.J., Matsuno K., King H., Artavanis-Tsakonas S.;  
 RT "Cytosolic interaction between Deltex and Notch ankyrin repeats  
 RT implicates Deltex in the Notch signaling pathway.";  
 RL Development 120:473-481 (1994).  
 RN [8]  
 RP INTERACTION WITH DX.  
 RX MEDLINE=95401878; PubMed=7671825;  
 RA Matsuno K., Diederich R.J., Go M.J., Blaumueller C.M.,  
 RA Artavanis-Tsakonas S.;  
 RT "Deltex acts as a positive regulator of Notch signaling through  
 RT interactions with the Notch ankyrin repeats.";  
 RL Development 121:2633-2644 (1995).  
 RN [9]  
 RP S3 CLEAVAGE BY PSN.  
 RX MEDLINE=99221487; PubMed=10206646;  
 RA Struhl G., Greenwald I.;  
 RT "Presenilin is required for activity and nuclear access of Notch in  
 RT Drosophila.";  
 RL Nature 398:522-525 (1999).  
 RN [10]  
 RP S3 CLEAVAGE BY PSN.  
 RX MEDLINE=99221488; PubMed=10206647;  
 RA Ye Y., Lukinova N., Fortini M.E.;  
 RT "Neurogenic phenotypes and altered Notch processing in Drosophila  
 RT Presenilin mutants.";  
 RL Nature 398:525-529 (1999).  
 RN [11]  
 RP S2 CLEAVAGE BY KUZ.  
 RX MEDLINE=21657146; PubMed=11799064;  
 RA Lieber T., Kidd S., Young M.W.;  
 RT "Kuzbanian-mediated cleavage of Drosophila Notch.";  
 RL Genes Dev. 16:209-221 (2002).  
 RN [12]  
 RP MUTANT MCD5.  
 RX MEDLINE=21575956; PubMed=11719214;  
 RA Ramin P., Knechumian K., Seugnet L., Arbogast N., Ackermann C.,  
 RA Heitzler P.;  
 RT "Novel Notch alleles reveal a Deltex-dependent pathway repressing  
 RT neural fate.";  
 RL Curr. Biol. 11:1729-1738 (2001).

RP MEDLINE=22256570; PubMed=12369105;  
RA Portin P.;  
RT "General outlines of the molecular genetics of the Notch signalling  
pathway in Drosophila melanogaster: a review.";  
RL Hereditas 136:89-96(2002).  
CC -!- FUNCTION: Signaling protein, which regulates, with both positive  
and negative signals, the differentiation of at least central and  
peripheral nervous system and eye, wing disk, oogenesis, segmental  
appendages such as antennae and legs, and muscles, through lateral  
inhibition or induction. Functions as a receptor for membrane-  
bound ligands Delta and Serrate to regulate cell-fate  
determination. Upon ligand activation, and releasing from the cell  
membrane, the Notch intracellular domain (NICD) forms a  
transcriptional activator complex with Su(H) (suppressor of  
hairless) and activates genes of the E(spl) complex. Essential for  
proper differentiation of ectoderm.  
CC -!- SUBUNIT: Interacts with Su(H) when activated. Interacts with Dx  
via its ANK repeats.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Upon activation and  
S3 cleavage, it is released from the cell membrane and enters into  
the nucleus in conjunction with Su(H).  
CC -!- PTM: Upon binding its ligands such as Delta or Serrate, it is  
cleaved (S2 cleavage) in its extracellular domain, close to the  
transmembrane domain. S2 cleavage is probably mediated by Kuz. It  
is then cleaved (S3 cleavage) downstream of its transmembrane  
domain, releasing it from the cell membrane. S3 cleavage requires  
Psn.  
CC -!- SIMILARITY: Belongs to the NOTCH family.  
CC -!- SIMILARITY: Contains 36 EGF-like domains.  
CC -!- SIMILARITY: Contains 3 Lin/Notch repeats.  
CC -!- SIMILARITY: Contains 6 ANK repeats.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
DR EMBL; M16152; AAB59220.1; -  
DR EMBL; M16153; AAB59220.1; JOINED.  
DR EMBL; M16149; AAB59220.1; JOINED.  
DR EMBL; M16150; AAB59220.1; JOINED.  
DR EMBL; M16151; AAB59220.1; JOINED.  
DR EMBL; K03508; AAB28725.1; -  
DR EMBL; M13689; AAB28725.1; JOINED.  
DR EMBL; K03507; AAB28725.1; JOINED.  
DR EMBL; AE003426; AAF45948.2; -  
DR EMBL; AL035436; CAB37610.1; -  
DR EMBL; AL035395; CAB37610.1; JOINED.  
DR EMBL; M12175; AAY74496.1; -  
DR EMBL; M16025; AAB28726.1; -  
Alignment Scores:  
Pred. No.: 0.0177 Length: 2703  
Score: 102.00 Matches: 25  
Percent Similarity: 42.25% Conservative: 5  
Best Local Similarity: 35.21% Mismatches: 29  
Query Match: 11.49% Indels: 12  
DB: 1 Gaps: 3  
US-09-773-476-294 (1-489) x NOTC\_DROME (1-2703)  
QY 170 CCTGTCTGAGTAGTATGCTGGCAATGTTACTTCTTTCAGGACAG----- 223  
Db 1229 ProCysGlnAsnGlyThrCysHisAspArgValMetAsnPheserCysSerPro 1248  
QY 224 -----CAGATTTCAGGCGCAAGGACCTTTTGCAATAGCAGC 268  
Db 1249 ProGlyThrMetGlyIleIleCysGluIleAsnLysAspCys-----Lys 1264

QY 269 CCAGAAATGTCTCTGAGAACGATCTTGTGCATCTGACGGTCTGCTGCTTTTTCAGTGC 328  
Db 1265 ProGlyAlaCysHisAsnGlySerCysIle---AspArgValGlyGlyPheGluCys 1283  
QY 329 GTTGTGCTGATGTTTCCATGATGATCAAGTGT 361  
Db 1284 ValCysGlnProGlyPheValGlyAlaArgCys 1294  
RESULT 7  
ID NTCL\_HUMAN STANDARD; PRT; 2556 AA.  
AC P46531;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Neurogenic locus notch homolog protein 1 precursor (Notch 1) (hnl)  
DE (Translocation-associated notch protein TAN-1).  
GN NOTCH1 OR TAN1.  
OS Homo sapiens (Human).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
CN NCBI\_TaxID=9606;  
[1]  
RC TISSUE=Brain;  
RA Mann R.S., Blaumüller C.M., Zagouras P.;  
RT "Complete human notch 1 (hnl) cDNA sequence.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
[2]  
RN SEQUENCE OF 1-2444 FROM N.A.  
RP MEDLINE=91347367; PubMed=1831692;  
RA Ellisen L.W., Bird J., West D.C., Soreng A.L., Reynolds T.C.,  
RA Smith S.D., Sklar J.;  
RT "TAN-1, the human homolog of the Drosophila notch gene, is broken by  
chromosomal translocations in T lymphoblastic neoplasms.";  
RL Cell 66:649-661(1991).  
[3]  
RP IDENTIFICATION OF LIGANDS.  
RX MEDLINE=99180765; PubMed=10079256;  
RA Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.L.,  
RA Banks A., Leiman J., Ward D., Ieh-Horowitz D., Artavanis-Taikonas S.;  
RT "Human ligands of the Notch receptor.";  
RL Am. J. Pathol. 154:785-794(1999).  
[4]  
RP INTERACTION WITH DTX1.  
RX MEDLINE=98250176; PubMed=9590294;  
RA Matsuno K., Eastman D., Mitsiades T., Quinn A.M., Carcanciu M.L.,  
RA Ordentlich P., Kadesch T., Artavanis-Taikonas S.;  
RT "Human deltex is a conserved regulator of Notch signalling.";  
RL Nat. Genet. 19:74-78(1998).  
CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands  
Jagged1, Jagged2 and Deltal to regulate cell-fate determination.  
CC Upon ligand activation through the released notch intracellular  
domain (NICD) it forms a transcriptional activator complex with  
RBP-J kappa and activates genes of the enhancer of split locus.  
CC Affects the implementation of differentiation, proliferation and  
apoptotic programs. May be important for normal lymphocyte  
function. In altered form, may contribute to transformation or  
progression in some T-cell neoplasms. Involved in the maturation  
of both CD4+ and CD8+ cells in the thymus (By similarity).  
CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-  
terminal fragment N(EC) which are probably linked by disulfide  
bonds (By similarity). Interacts with DTX1 and DTX2.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following  
proteolytical processing NICD is translocated to the nucleus (By  
similarity).  
CC -!- TISSUE SPECIFICITY: In fetal tissues most abundant in spleen,  
brain stem and lung. Also present in most adult tissues where it  
is found mainly in lymphoid tissues.  
CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form  
which is proteolytically cleaved by a furin-like convertase in the  
trans-Golgi network before it reaches the plasma membrane to yield







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US-09-773-476-294 (1-489) x NTC1_HUMAN (1-2556)
QY 53 TTACAGGCTTACTGCT-----ATTATCATAGACCTTCAG-----GCAATCCT 97
Dd ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
441 LeuGlnGlyTyThrGlyProArgCysGluIleAspValAsnGluCysValSerAsnPro 460
QY 98 CTCAGAGTATTGGCCCAACCTTCCTGGTGTACTACCTGCAGACTCTGATCTA 157
Dd ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
461 CysGlnAsnAsp---AlaThrCysLeuAspGlnIleGlyGluPheGlnCysMetCysMet 479
QY 158 CCA-----CAAGATGTTCCCTGT 175
Dd ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
480 ProGlyTyThrGlyValHisCysGluValAsnThrAspGluCysAlaSerSerProCys 499
QY 176 CTGGAGGTAGTAATCCCTGGACATGTTACTCTTTCAAGGACAAG----- 223
Dd ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
500 LeuHisAsnGlyArgCysLeuAspValAsnGluPheGlnCysGluCysProThrGly 519
QY 224 -----CAGATTGCAAGGCAAGGACCTTTCGAATGACACTGGAAGCCAGAA 274
Dd ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
520 PheThrGlyHisLeuCysGlnIleAspValAspGluCysAlaSerThr----- 535
QY 275 ATGTGCTCTGAGAACGGATCTGTGCATCTGACGGTCCCTGCTTTGCGAGTGGCTTGT 334
Dd ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
536 ProCys---LysAsnGlyAlaLysCysLeuAspGlyProAsnThrTyThrCysValCys 554
QY 335 GCTGATGTTTCATGATACAAAGT-----ATGGCAGGCTCATTTCTACTGCTTATGTTCTTTGG 400
Dd ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
555 ThrGluGlyTyThrGlyThrHisCysGluValAspIleAspGluCysAspProAspPro 574
QY 362 -----ATGGCAGGCTCATTTCTACTGCTTATGTTCTTTGG 400
Dd ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
575 CysHisTyThrGlySerCysLysAsp---GlyValAlaThrPheThrCysLeuCysArgProG 594
QY 401 ATTC 404
Dd ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
594 Tyr 595

RESULT 8
NTC3_RAT
ID NTC3_RAT STANDARD; PRT; 2319 AA.
AC Q9R172;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurogenic locus notch homolog protein 3 precursor (Notch 3).
GN NOTCH3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RA Hartunians T., Boulter J., Weinmaster G., Schanen N.C.;
RT "Rattus norvegicus mRNA for Notch 3.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP FUNCTION.
RX MEDLINE=21094508; PubMed=11182080;
RA Tanigaki K., Nogaki F., Takanashi J., Tashiro K., Kurooka H.,
RA Honjo T.;
RT "Notch1 and Notch3 instructively restrict bFGF-responsive multipotent
RT neural progenitor cells to an astroglial fate.";
RL Neuron 29:45-55(2001).
RN [3]
RP TISSUE SPECIFICITY.
RX MEDLINE=21331789; PubMed=11438922;
RA Irvin D.K., Zurcher S.D., Nguyen T., Weinmaster G., Kornblum H.I.;
RT "Expression patterns of Notch1, Notch2, and Notch3 suggest multiple
RT functional roles for the Notch-DSL signaling system during brain
RT development.";
RL J. Comp. Neurol. 436:167-181(2001).
```

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-!- FUNCTION: Functions as a receptor for membrane-bound ligands
Jagged1, Jagged2 and Deltal to regulate cell-fate determination.
Upon ligand activation through the released notch intracellular
domain (NICD) it forms a transcriptional activator complex with
RBP-J kappa and activates genes of the enhancer of split locus.
Affects the implementation of differentiation, proliferation and
apoptotic programs (By similarity). Acts instructively to control
the cell fate determination of CNS multipotent progenitor cells,
resulting in astroglial induction and neuron/oligodendrocyte
suppression.
-!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
terminal fragment N(EC) which are probably linked by disulfide
bonds (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein. Following
proteolytical processing NICD is translocated to the nucleus.
-!- TISSUE SPECIFICITY: Expressed in postnatal central nervous system
(CNS) germinal zones and, in early postnatal life, within
numerous cells throughout the CNS. It is more highly localized
to ventricular germinal zones.
-!- PTM: Synthesized in the endoplasmic reticulum as an inactive form
which is proteolytically cleaved by a furin-like convertase in the
trans-Golgi network before it reaches the plasma membrane to yield
an active, ligand-accessible form. Cleavage results in a C-
terminal fragment N(TM) and a N-terminal fragment N(EC). Following
ligand binding, it is cleaved by TNF-alpha converting enzyme
(TACE) to yield a membrane-associated intermediate fragment called
notch extracellular truncation (NEXT). This fragment is then
cleaved by presenilin dependent gamma-secretase to release a
notch-derived peptide containing the intracellular domain (NICD)
from the membrane (By similarity).
-!- PTM: Phosphorylated (By similarity).
-!- SIMILARITY: Belongs to the NOTCH family.
-!- SIMILARITY: Contains 34 EGF-like domains.
-!- SIMILARITY: Contains 3 Lin/Notch repeats.
-!- SIMILARITY: Contains 5 ANK repeats.

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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@sib-sib.ch).

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EMBL; AF164486; AAD46653.2; ..
HSSP; P00740; 1EDM
InterPro; IPR002110; ANK.
InterPro; IPR000152; Asx_Hydroxyl_S.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR006209; EGF_Like.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR008297; Notch.
InterPro; IPR000800; Notch_dom.
Pfam; PF00023; ank; 6.
Pfam; PF00066; notch; 3.
Pfam; PIRS002279; Notch; 1.
PRINTS; PR00010; EGFBLD.
PRINTS; PR00011; EGF_LAMININ.
PRINTS; PR01452; NOTCH.
SMART; SMO0248; ANK; 6.
SMART; SMO0179; EGF_CA; 20.
SMART; SMO0004; NL; 3.
PROSITE; PS50297; ANK_REPEAT_REGION; 1.
PROSITE; PS50088; ANK_REPEAT; 4.
PROSITE; PS00010; ASX_HYDROXYL; 18.
PROSITE; PS00022; EGF_1; 33.
PROSITE; PS01186; EGF_2; 26.
PROSITE; PS50026; EGF_3; 34.
PROSITE; PS01187; EGF_CA; 16.
Receptor; Transcription regulation; Activator; Differentiation;
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KW Developmental protein; Repeat; ANK repeat; EGF-like domain;  
 Transmembrane; Glycoprotein; Signal; Phosphorylation.  
 FT SIGNAL 1 40 POTENTIAL.

FT CHAIN 41 2319 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 3.  
 FT CHAIN 1631 2319 NOTCH EXTRACELLULAR TRUNCATION (BY  
 SIMILARITY).

FT CHAIN 1664 2319 NOTCH INTRACELLULAR DOMAIN (BY  
 SIMILARITY).

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 SIMILARITY).

FT DISULFID 280 293 BY SIMILARITY.

FT DISULFID 287 302 BY SIMILARITY.

FT DISULFID 304 313 BY SIMILARITY.

FT DISULFID 320 331 BY SIMILARITY.

FT DISULFID 325 340 BY SIMILARITY.

FT DISULFID 342 351 BY SIMILARITY.

FT DISULFID 357 368 BY SIMILARITY.

FT DISULFID 362 379 BY SIMILARITY.

FT DISULFID 381 390 BY SIMILARITY.

FT DISULFID 397 410 BY SIMILARITY.

FT DISULFID 404 419 BY SIMILARITY.

FT DISULFID 421 430 BY SIMILARITY.

FT DISULFID 437 448 BY SIMILARITY.

FT DISULFID 442 457 BY SIMILARITY.

FT DISULFID 459 468 BY SIMILARITY.

FT DISULFID 475 486 BY SIMILARITY.

FT DISULFID 480 495 BY SIMILARITY.

FT DISULFID 497 506 BY SIMILARITY.

FT DISULFID 513 524 BY SIMILARITY.

FT DISULFID 518 533 BY SIMILARITY.

FT DISULFID 535 544 BY SIMILARITY.

FT DISULFID 551 561 BY SIMILARITY.

Alignment Scores:

Pred. No.: 0.028 Length: 2319

Score: 100.00 Matches: 28

Percent Similarity: 38.54% Conservative: 9

Best Local Similarity: 29.17% Mismatches: 23

Query Match: 11.26% Indels: 36

DB: 1 Gaps: 6

US-09-773-476-294 (1-489) x NTC3\_RAT (1-2319)

QY 140 CTGCAGACTCTGATACACCAAGATGTCCTCTG-----175

Db 690 LeuProPLeuCysLeuProAlaHisProCysAlaHisLysProCysSerHisGly 709

QY 176 -----CCTGGAGGTAGTAATGCTGGGCAACATGTTCTTTCAAGGAC 220

Db 710 ValCysHisAspAlaProGlyGlyPheGlnCys-----720

QY 221 AAGCAGATTTC-----CAAGGGCAAGGACCTTTGCAATAGCATTGGAAGC 268

Db 721 -----ValCysAspProGlyTrpSerGlyProArg-----CysSerGlnSerLeuAla 736

QY 269 CCGAATATGTCCTCTGAG-----AACGGATCTTGTGCATCTGACGTCCT 313

Db 737 ProAspAlaCysGluSerGlnProCysGlnAlaGlyGlyThrCysThrSerAspGlyIle 756

QY 314 GGTCTTTTGCAGTGGCTTGTGCTGATGTTCCATGATACAAAGTGT 361

Db 757 Gly---PheHisCysThrCysAlaProGlyGlyPheGlnGlyHisGlnCys 771

RESULT 9

JAG3 BRARE

ID JAG3 BRARE STANDARD; PRT; 1213 AA.

AC Q90Y54.

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Jagged 3 precursor (Jagged3).

GN JAG3.

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI\_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RA Oda T., Chandrasekharappa S.C.;

RT "Isolation, characterization and expression analysis of Zebrafish

RT Jagged Genes.";

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

FT	DISULFID	303	319	BY SIMILARITY.
FT	DISULFID	321	330	BY SIMILARITY.
FT	DISULFID	337	348	BY SIMILARITY.
FT	DISULFID	342	357	BY SIMILARITY.
FT	DISULFID	359	368	BY SIMILARITY.
FT	DISULFID	375	386	BY SIMILARITY.
FT	DISULFID	380	395	BY SIMILARITY.
FT	DISULFID	397	406	BY SIMILARITY.
FT	DISULFID	413	424	BY SIMILARITY.
FT	DISULFID	418	433	BY SIMILARITY.
FT	DISULFID	435	444	BY SIMILARITY.
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FT	DISULFID	548	557	BY SIMILARITY.
FT	DISULFID	630	641	BY SIMILARITY.
FT	DISULFID	635	650	BY SIMILARITY.
FT	DISULFID	652	661	BY SIMILARITY.
FT	DISULFID	668	679	BY SIMILARITY.
FT	DISULFID	673	688	BY SIMILARITY.
FT	DISULFID	690	699	BY SIMILARITY.
FT	DISULFID	706	717	BY SIMILARITY.
FT	DISULFID	711	726	BY SIMILARITY.
FT	DISULFID	728	737	BY SIMILARITY.
FT	DISULFID	783	794	BY SIMILARITY.
FT	DISULFID	788	803	BY SIMILARITY.
FT	DISULFID	805	814	BY SIMILARITY.
FT	DISULFID	821	832	BY SIMILARITY.
FT	DISULFID	826	841	BY SIMILARITY.
FT	DISULFID	843	852	BY SIMILARITY.
FT	DOMAIN	938	941	POLY-PRO.
FT	CARBOHYD	139	139	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	214	214	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	556	556	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	742	742	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	957	957	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	988	988	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1042	1042	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	SEQUENCE	1213	AA; 133365 MW; 5C5F16A7E20D9534	CRC64;
US-09-773-476-294	(1-489) x JAG3_BRARE	(1-1213)		
QY	224	CAGATTGCCAAGGGCAAGGACCTTTTGCATAGCACTGGAGCCGCAAGTAATGTGCT	283	
Db	288	GlnLeuCys-----AspLysAspLeu---AsnTyrCysGlyThrHisGlnProCysLeu	304	
QY	284	GAGAACCGATCTGTGCATCTGACGGTCTGCTCTTTTGGTCAGTGGCTTTGGCTGATGGT	343	
Db	305	AsnGlyGlyThrCysSerAsnThrGlyProAspLysTyrGlnCysSerCysGluAspGly	324	
QY	344	TTCCATCGATACAAAGTGATGAGCGAGGCTCAT	377	
Db	325	TyrSerGlyValAsnCysGluArg-AlaGluHisAlaCysLeuSerAsnProCysAlaAs	344	
QY	378	-----TTTCACTGCTTATGTTCTTTGGGATTC	404	
Db	344	nGlyGlyThrCysLysGluThrSerGlnGlyThrGlyCysHisCysAlaIleGlyTrp	363	

Alignment Scores:

Pred. No.:	0.0314	Length:	1213
Score:	99.00	Matches:	23
Percent Similarity:	43.75%	Conservative:	12
Best Local Similarity:	28.75%	Mismatches:	22
Query Match:	11.15%	Indels:	23
DB:	1	Gaps:	3

RESULT 10

NTC4 MOUSE

NTC4\_MOUSE STANDARD; PRT; 1964 AA.  
AC P31695; O35442; O88314; Q62389; Q62390; Q9RIW9; Q9RI1X0;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neurogenic locus notch homolog protein 4 precursor (Notch 4)  
GN [Contains: transforming protein Int-3].  
GN NOTCH4 OR INT3 OR INT-3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92194507; PubMed=1312643;  
RA Robbins J., Blondel B.J., Gallahan D., Callahan R.;  
RT "Mouse mammary tumor gene int-3: a member of the notch gene family  
RT transforms mammary epithelial cells.";  
RL J. Virol. 66:2594-2599(1992).  
RN [2]  
RP REVISIONS, SEQUENCE FROM N.A.  
RX MEDLINE=97294599; PubMed=9150355;  
RA Gallahan D., Callahan R.;  
RT "The mouse mammary tumor associated gene INT3 is a unique member of  
RT the NOTCH gene family (NOTCH4).";  
RL Oncogene 14:1883-1890(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Lung, and Testis;  
RC MEDLINE=96281668; PubMed=8681805;  
RA Uytendaele H., Marazzi G., Wu G., Van Q., Sassoon D., Kitajewski J.;  
RT "Notch4/int-3, a mammary proto-oncogene, is an endothelial  
RT cell-specific mammalian Notch gene.";  
RL Development 122:2251-2259(1996).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX Rowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,  
RA Loretz C., Schmidt S., Tipton S., Traicoff R., Zackrone K., Hood L.;  
RT "Sequence of the mouse major histocompatibility locus class III  
RT region.";  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 1436-1600 FROM N.A.  
RX MEDLINE=99252212; PubMed=10233982;  
RA Lee J.-S., Haruna T., Ishimoto A., Honjo T., Yanagawa S.-I.;  
RT "intracisternal type A particle-mediated activation of the Notch4/int3  
RT gene in a mouse mammary tumor: generation of truncated Notch4/int3  
RT mRNAs by retroviral splicing events.";  
RL J. Virol. 73:5166-5171(1999).  
RN [6]  
RP FUNCTION.  
RX MEDLINE=21244657; PubMed=11344305;  
RA Uytendaele H., Ho J., Rossant J., Kitajewski J.;  
RT "Vascular patterning defects associated with expression of activated  
RT Notch4 in embryonic endothelium.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:5643-5648(2001).  
RN [7]  
RP SEQUENCE OF 1463-1964, POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS  
OF VAL-1463  
RX MEDLINE=21523956; PubMed=11518718;  
RA Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;  
RT "Murine notch homologs (N1-4) undergo presenilin-dependent  
RT proteolysis.";  
RL J. Biol. Chem. 276:40268-40273(2001).  
RN [8]  
RP POST-TRANSLATIONAL PROCESSING.  
RX MEDLINE=21374376; PubMed=11459941;  
RA Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;  
RT "Conservation of the biochemical mechanisms of signal transduction  
RT among mammalian Notch family members.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).  
CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands  
Jagged1, Jagged2 and Delta to regulate cell-fate determination.

CC Upon ligand activation through the released notch intracellular  
CC domain (NICD) it forms a transcriptional activator complex with  
CC RBP-J kappa and activates genes of the enhancer of split locus.  
CC Affects the implementation of differentiation, proliferation and  
CC apoptotic programs (By similarity). May regulate branching  
CC morphogenesis in the developing vascular system.  
CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-  
CC terminal fragment N(EC) which are probably linked by disulfide  
CC bonds.  
CC -!- CELLULAR LOCATION: Type I membrane protein. Following  
CC proteolytical processing NICD is translocated to the nucleus.  
CC -!- TISSUE SPECIFICITY: Highly expressed in lung, moderately in heart  
CC kidney, and at lower levels in the ovary and skeletal muscle. A  
CC very low expression is seen in the brain, intestine, liver and  
CC testis.  
CC -!- DEVELOPMENTAL STAGE: Highly expressed in endothelial cells during  
CC embryonic development from 9.0 dpc.  
CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form  
CC which is proteolytically cleaved by a furin-like convertase in the  
CC trans-Golgi network before it reaches the plasma membrane to yield  
CC an active, ligand-accessible form. Cleavage results in a C-  
CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following  
CC ligand binding, it is cleaved by TNF-alpha converting enzyme  
CC (TACE) to yield a membrane-associated intermediate fragment called  
CC notch extracellular truncation (NEXT). This fragment is then  
CC cleaved by presenilin dependent gamma-secretase to release a  
CC notch-derived peptide containing the intracellular domain (NICD)  
CC from the membrane.  
CC -!- PTM: Phosphorylated.  
CC -!- DISEASE: Loss of the extracellular domain causes constitutive  
CC activation of the Notch protein, which leads to hyperproliferation  
CC of glandular epithelial tissues and development of mammary  
CC carcinomas.  
CC -!- SIMILARITY: Belongs to the NOTCH family.  
CC -!- SIMILARITY: Contains 29 EGF-like domains.  
CC -!- SIMILARITY: Contains 3 Lin/Notch repeats.  
CC -!- SIMILARITY: Contains 5 ANK repeats.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
CC -----  
CC EMBL; M80456; AAB38377.1; -;  
CC EMBL; U43691; AAC52630.1; -;  
CC EMBL; U43691; AAC52631.1; -;  
CC EMBL; AF030001; AAB82004.1; -;  
CC EMBL; AB016771; BAA32281.1; ALT\_SEQ.  
CC EMBL; AB016772; BAA32283.1; ALT\_INIT.  
CC EMBL; AB016773; BAA32284.1; ALT\_INIT.  
CC EMBL; AB016774; BAA32285.1; -;  
CC PIR; A38072; TVMVT3.  
CC PIR; T09059; T09059.  
CC HSSP; P08709; 1BF9.  
CC MGD; MGI:107471; Notch4.  
CC InterPro; IPR002110; ANK.  
CC InterPro; IPR000152; Asx\_hydroxyl\_S.  
CC InterPro; IPR000742; EGF\_2.  
CC InterPro; IPR001881; EGF\_Ca.  
CC InterPro; IPR001438; EGF\_II.  
CC InterPro; IPR006209; EGF\_like.  
CC InterPro; IPR002049; Laminin\_EGF.  
CC InterPro; IPR008297; Notch\_dom.  
CC InterPro; IPR008800; Notch\_dom.  
CC Pfam; PF00023; ank; 6.  
CC Pfam; PF00008; EGF; 27.  
CC Pfam; PF00066; notch; 2.  
CC PIRSF; PIRSF002279; Notch; 1.  
CC PRINTS; PR00010; EGFBL00D.  
CC PRINTS; PR00011; EGFLAMININ.

DR PRINTS; PRO1452; NOTCH.  
 DR SMART; SM00248; ANK; 6.  
 DR SMART; SM00179; EGF\_CA; 11.  
 DR SMART; SM00004; NL; 2.  
 DR PROSITE; PS00297; ANK REP REGION; 1.  
 DR PROSITE; PS00088; ANK REPEAT; 5.  
 DR PROSITE; PS00010; ASX-HYDROXYL; 11.  
 DR PROSITE; PS00022; EGF\_1; 28.  
 DR PROSITE; PS01186; EGF\_2; 21.  
 DR PROSITE; PS00026; EGF\_3; 27.  
 DR PROSITE; PS01187; EGF\_CA; 9.  
 KW Receptor; Transcription regulation; Activator; Differentiation;  
 KW Developmental protein; Repeat; ANK repeat; EGF-like domain;  
 KW Transmembrane; Glycoprotein; Signal; Phosphorylation; Proto-oncogene.  
 FT SIGNAL 1 20  
 FT CHAIN 21 1964  
 FT CHAIN 1411 1964  
 FT CHAIN 1428 1964  
 FT CHAIN 1463 1964  
 FT DOMAIN 21 1443  
 FT DOMAIN 1444 1464  
 FT TRANSMEM 1444 1464  
 FT DOMAIN 1465 1964  
 FT DOMAIN 21 60  
 FT DOMAIN 61 112  
 FT DOMAIN 115 152  
 FT DOMAIN 153 189  
 FT DOMAIN 191 229  
 FT DOMAIN 231 271  
 FT DOMAIN 273 309  
 FT DOMAIN 311 350  
 FT DOMAIN 352 388  
 FT DOMAIN 389 427  
 FT DOMAIN 429 470  
 FT DOMAIN 472 508  
 FT DOMAIN 510 546  
 FT DOMAIN 548 594  
 FT DOMAIN 596 632  
 FT DOMAIN 633 656  
 FT DOMAIN 658 686  
 FT DOMAIN 688 724  
 FT DOMAIN 726 762  
 FT DOMAIN 764 800  
 FT DOMAIN 803 839  
 FT DOMAIN 841 877  
 FT DOMAIN 878 924  
 FT DOMAIN 926 962  
 FT DOMAIN 964 1000  
 FT DOMAIN 1002 1040  
 FT DOMAIN 1042 1081  
 FT DOMAIN 1083 1122  
 FT DOMAIN 1126 1167  
 FT REPEAT 1168 1208  
 FT REPEAT 1209 1242  
 FT REPEAT 1243 1282

Alignment Scores:  
 Pred. No.: 0.0345  
 Score: 99.00  
 Percent Similarity: 34.87%  
 Best Local Similarity: 24.34%  
 Query Match: 11.15%  
 DB: 1

US-09-773-476-294 (1-489) x NTC4\_MOUSE (1-1964)  
 QY 41 GGTCACAACTTT-----TTACAGCGTTTACTGCTATTATCATGACCTTCAG 88  
 Db 860 GlyProSerPheGlnCysLeuGlnGlyTrpThrGlyAlaLeuCysAspPhe--- 878  
 QY 89 GCAAAATCTCTCAAGATGATTGGCCAAACACTTCGGTGGTCTACTGAGTGGAGCT 148  
 Db 879 -----ProLeuSerCysGlnMetAlaAlaMetSerGlnGlyLe---GluileSerGly 895

QY 149 CTGATACTACCACAGATGTTCCCTGCTGGAGGTAGTAACTGCTGGGACATGTTACT 208  
 Db 896 Leu-----CysGlnAsnGlyGlyLeuCysIleAspThrGlySer 908  
 QY 209 TCTTTCAAGGACAAAG-----CAGATTGTCACAGGCGCAAGGGAC 247  
 Db 909 SerTy-PheCysArgCysProGlyPheGlnGlyLysLeuCysGlnAspAsnMetAsn 928  
 QY 248 CTTTGCAATAGCACTGGAGCCAGAAATGTCCTGAGACGGAATCTTGTCATCTGAC 307  
 Db 929 ProCys-----GluProAsnProCysHisHisGlySerThrCysValProGln 944  
 QY 308 GGTCCCTGGTCTTTGTCAGTCGCTTTGTGTGATGGTTTCCATGGATCAAGTGT----- 361  
 Db 945 ProSerGlyTyVal---CysGlnCysAlaProGlyTyrcGluGlyGlnAsnCysSerLys 963  
 QY 362 -----ATGAGGCAG 370  
 Db 964 ValLeuGluAlaCysGlnSerGlnProCysHisAsnHisGlyThrCysThrSerArgPro 983  
 QY 371 GGTCATTTTCACTGCTTATGTTCTTTGGGATTC 404  
 Db 984 GlyGly-PheHisCysAlaCysProGlyPhe 994

RESULT 11  
 NTC4 HUMAN  
 ID NTC4\_HUMAN STANDARD; PRT; 2003 AA.  
 AC Q99456; Q00306; Q99458; Q99940; Q9H3S8; Q9UII9; Q9UIJ0;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neurogenic locus notch homolog protein 4 precursor (Notch 4)  
 DE (hntch4).  
 GN NOTCH4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND POLYMORPHISM OF POLY-LEU.  
 RC TISSUE=Placenta;  
 RX MEDLINE=97311416; PubMed=9168133;  
 RA Sugaya K., Sasanuma S.-I., Nohata J., Kimura T., Fukagawa T.,  
 RA Nakamura Y., Ando A., Inoko H., Ikemura T., Mita K.;  
 RA "Gene organization of human NOTCH4 and (CTG)n polymorphism in this  
 RA human counterpart gene of mouse proto-oncogene Int3.";  
 RL Gene 189:235-244(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RC TISSUE=Bone marrow, and Heart;  
 RX MEDLINE=98360091; PubMed=9693032;  
 RA Li L., Huang G.M., Banta A.B., Deng Y., Smith T., Dong P.,  
 RA Friedman C., Chen L., Trask B.J., Spies T., Rowen L., Hood L.;  
 RA "Cloning, characterization, and the complete 56.8-kilobase DNA  
 RA sequence of the human NOTCH4 gene.";  
 RL Genomics 51:45-58(1998).  
 RN [3]  
 RP SEQUENCE OF 1-503 FROM N.A., AND VARIANTS GLN-117 AND GLN-317.  
 RX MEDLINE=99180765; PubMed=10079256;  
 RA Miyagawa T., Tokunaga K., Hojcho H.;  
 RA "Human notch4 gene variant.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP IDENTIFICATION OF LIGANDS.  
 RX MEDLINE=99180765; PubMed=10079256;  
 RA Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,  
 RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Teakonas S.;  
 RL "Human ligands of the Notch receptor.";  
 RL Am. J. Pathol. 154:785-794(1999).  
 CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands  
 CC Jagged1, Jagged2 and Delta1 to regulate cell-fate determination.  
 CC Upon ligand activation through the released notch intracellular  
 CC domain (NICD) it forms a transcriptional activator complex with  
 CC RBP-J kappa and activates genes of the enhancer of split locus.



FT	DISULFID	122	133	BY SIMILARITY.
FT	DISULFID	127	143	BY SIMILARITY.
FT	DISULFID	145	154	BY SIMILARITY.
FT	DISULFID	160	171	BY SIMILARITY.
FT	DISULFID	165	180	BY SIMILARITY.
FT	DISULFID	182	191	BY SIMILARITY.
FT	DISULFID	198	211	BY SIMILARITY.
Alignment Scores:				
Pred. No.:	0.0347	Length:	2003	
Score:	99.00	Matches:	32	
Percent Similarity:	37.7%	Conservative:	8	
Best Local Similarity:	30.1%	Mismatches:	34	
Query Match:	11.15%	Indels:	32	
DB:	1	Gaps:	6	
US-09-773-476-294 (1-489) x NTC4_HUMAN (1-2003)				
QY	107	GATTGGCCACACCTTCGCGGGTTACTACGTCGACACTCTGATACCTACCA	----- 160	
DB	530	AspLeuLeuAsnGlyPhe		
QY	161	-----CAAGATGTT		
DB	544	SerGlyThrArgCysGluGluAspLeuAspGluCysArgSerProCysAlaAsnGly		
QY	185	AGTAATGCTGGGACAACTTCTTCTTCAAGGCAAGCAGATT	----- 229	
DB	564	GlyGlnCysGlnAspGlnProGlyAlaPheHscysLysCysLeuProGlyPheGluGly		
QY	230	-----TGCCAGGGCAAGGACCTTTCATAGCAGCTGGAAGCCAGAAATGTCCT	283	
DB	584	ProArgCysGlnThrGluValAspGluCysLeuSer		
QY	284	GAGAACGGATCTGTGCATCTGACGCTCTGCTGCTTTTCAGTGGGTTTGCTGATGT	343	
DB	600	ValGlyAlaSerCysLeu---AspLeuProGlyAlaPhePheCysLeuCysProSerGly	618	
QY	344	TTCCATGGATACAAAGTGT	361	
DB	619	PheThrGlyGlnLeuCys	624	

RESULT 12

LTBS\_MOUSE STANDARD; PRT; 1389 AA.

AC Q8CG18; Q8ENW7; Q8CF5; Q8CIR0;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Latent transforming growth factor beta binding protein, isoform 1S precursor (LTBP-1) (Transforming growth factor beta-1 binding protein 1) (TGF-beta1-BP-1).

GN LTBP1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22597538; PubMed=12711388;

RA Noguera I., Obata H., Gualandris A., Cowin P., Rifkin D.B.;

RT "Molecular cloning of the mouse Ltbp-1 gene reveals tissue specific expression of alternatively spliced forms.";

RL Gene 308.31-41(2003).

RN [2]

RP SEQUENCE FROM N.A.

RX STRAIN=129/SVJ;

RX MEDLINE=22597539; PubMed=12711389;

RA Weiskirchen R., Moser M., Guenther K., Weiskirchen S., Gressner A.M.;

RT "The murine latent transforming growth factor-beta binding protein (ltbp-1) is alternatively spliced, and maps to a region syntenic to human chromosome xp21-22.";

RL Gene 308.43-52(2003).

[3]

SEQUENCE OF 788-1389 FROM N.A.

STRAIN=C57BL/6J; TISSUE=Aorta, Liver, and Vein;

MEDLINE=22354683; PubMed=12466851;

OKazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nakai I., Osato N., Saito K., Suzuki H., Yanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Brad D., Brusica V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Randel A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

CC -!- SUBUNIT: The large latent complex of TGF-beta1 from platelets is composed of the TGF-beta1 molecule noncovalently associated with a disulfide-bonded complex of a dimer of the N-terminal propeptide of the TGF-beta1 precursor and a third component denoted TGF-beta1-BP. TGF-beta1-BP does not bind directly to active TGF-BETA1. Binds to fibrillin (By similarity).

CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1S;

CC IsoId=Q8CG18-1; Sequence=Displayed;

CC Name=1L;

CC IsoId=Q8CG19-1; Sequence=External;

CC -!- PTM: Contains hydroxylated asparagine residues (By similarity).

CC -!- PTM: The N-terminus is blocked (By similarity).

CC -!- SIMILARITY: Contains 16 EGF-like domains.

CC -----

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CC -----

DR EMBL; AF346455; AAN77251.1;

DR EMBL; AF346438; AAN77251.1; JOINED.

DR EMBL; AF346439; AAN77251.1; JOINED.

DR EMBL; AF346440; AAN77251.1; JOINED.

DR EMBL; AF346441; AAN77251.1; JOINED.

DR EMBL; AF346442; AAN77251.1; JOINED.

DR EMBL; AF346443; AAN77251.1; JOINED.

DR EMBL; AF346444; AAN77251.1; JOINED.

DR EMBL; AF346445; AAN77251.1; JOINED.

DR EMBL; AF346446; AAN77251.1; JOINED.

DR EMBL; AF346447; AAN77251.1; JOINED.

DR EMBL; AF346448; AAN77251.1; JOINED.

DR EMBL; AF346449; AAN77251.1; JOINED.

DR EMBL; AF346450; AAN77251.1; JOINED.

DR EMBL; AF346451; AAN77251.1; JOINED.

DR EMBL; AF346452; AAN77251.1; JOINED.  
 DR EMBL; AF346453; AAN77251.1; JOINED.  
 DR EMBL; AF346454; AAN77251.1; JOINED.  
 DR EMBL; AF346455; AAN77251.1; JOINED.  
 DR EMBL; AF346456; AAN77251.1; JOINED.  
 DR EMBL; AF346457; AAN77251.1; JOINED.  
 DR EMBL; AF346458; AAN77251.1; JOINED.  
 DR EMBL; AF346459; AAN77251.1; JOINED.  
 DR EMBL; AF346460; AAN77251.1; JOINED.  
 DR EMBL; AF346461; AAN77251.1; JOINED.  
 DR EMBL; AF346462; AAN77251.1; JOINED.  
 DR EMBL; AF346463; AAN77251.1; JOINED.  
 DR EMBL; AF346464; AAN77251.1; JOINED.  
 DR EMBL; AY143161; AAN38831.1; ALT\_SEQ.  
 DR EMBL; AK080024; BAC37808.1; -.  
 DR MGD; MGI:109151; Ltbp1.  
 DR GO; GO:0005578; C:extracellular matrix; IDA.  
 DR InterPro; IPR00152; Asx\_hydroxyl\_S.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR002212; Fibril-assoc.  
 DR InterPro; IPR006210; IEGF.  
 DR Pfam; PF00008; EGF; 15.  
 DR Pfam; PF00683; TB; 4.  
 DR SMART; SM00181; EGF; 17.  
 DR SMART; SM00179; EGF\_Ca; 16.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 13.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 11.  
 DR PROSITE; PS50025; EGF\_3; 13.  
 DR PROSITE; PS01187; EGF\_Ca; 15.  
 DR Growth factor binding; Repeat; EGF-like domain;  
 KW Hydroxylation; Signal; Glycoprotein;  
 KW Alternative splicing.  
 FT SIGNAL 1 19  
 FT CHAIN 20 1389  
 FT DOMAIN 295 335  
 FT REPEAT 343 408  
 FT DOMAIN 542 583  
 FT DOMAIN 584 625  
 FT DOMAIN 626 666  
 FT DOMAIN 667 706  
 FT DOMAIN 707 747  
 FT DOMAIN 748 788  
 FT DOMAIN 789 829  
 FT DOMAIN 830 870  
 FT DOMAIN 871 912  
 FT DOMAIN 913 954  
 FT DOMAIN 955 997  
 FT REPEAT 1012 1079  
 FT DOMAIN 1092 1134  
 FT DOMAIN 1135 1175  
 FT REPEAT 1185 1257  
 FT DOMAIN 1289 1330  
 FT DOMAIN 1330 1374  
 FT DISULFID 299 310

FT DISULFID 305 319 POTENTIAL.  
 FT DISULFID 321 334 POTENTIAL.  
 FT DISULFID 346 358 POTENTIAL.  
 FT DISULFID 353 367 POTENTIAL.  
 FT DISULFID 369 382 POTENTIAL.  
 FT DISULFID 388 400 POTENTIAL.  
 FT DISULFID 395 409 POTENTIAL.  
 FT DISULFID 411 424 POTENTIAL.  
 FT DISULFID 430 441 POTENTIAL.  
 FT DISULFID 436 450 POTENTIAL.  
 FT DISULFID 453 465 POTENTIAL.  
 FT DISULFID 471 482 POTENTIAL.  
 FT DISULFID 477 491 POTENTIAL.  
 FT DISULFID 494 505 POTENTIAL.  
 FT DISULFID 511 522 POTENTIAL.  
 FT DISULFID 517 531 POTENTIAL.  
 FT DISULFID 533 546 POTENTIAL.  
 FT DISULFID 552 563 POTENTIAL.  
 FT DISULFID 571 582 POTENTIAL.  
 FT DISULFID 577 591 POTENTIAL.  
 FT DISULFID 594 605 POTENTIAL.  
 FT DISULFID 611 624 POTENTIAL.  
 FT DISULFID 630 641 POTENTIAL.  
 FT DISULFID 636 650 POTENTIAL.  
 FT DISULFID 653 665 POTENTIAL.  
 FT DISULFID 671 682 POTENTIAL.  
 FT DISULFID 677 691 POTENTIAL.  
 FT DISULFID 694 705 POTENTIAL.  
 FT DISULFID 711 722 POTENTIAL.  
 FT DISULFID 717 731 POTENTIAL.  
 FT DISULFID 733 746 POTENTIAL.  
 FT DISULFID 752 763 POTENTIAL.  
 FT DISULFID 758 772 POTENTIAL.  
 FT DISULFID 774 787 POTENTIAL.  
 FT DISULFID 793 804 POTENTIAL.  
 FT DISULFID 799 813 POTENTIAL.  
 FT DISULFID 815 828 POTENTIAL.  
 FT DISULFID 834 846 POTENTIAL.  
 FT DISULFID 841 855 POTENTIAL.  
 Alignment Scores:  
 Pred. No.: 0.0364 Length: 1389  
 Score: 98.50 Matches: 30  
 Percent Similarity: 34.58% Conservative: 7  
 Best Local Similarity: 28.04% Mismatches: 34  
 Query Match: 11.09% Indels: 36  
 DB: 1 Gaps: 4  
 US-09-773-476-294 (1-489) x LTBS\_MOUSE (1-1389)  
 QY 164 GATGTCCTCTCTGGAGGTAGTAATGCTGGGACAACTGTTACTTCTTTCAGGCAAG 223  
 Db 854 AspCysThrCysProAspGlyPheGlnLeuAsnAspAsn----- 866  
 QY 224 CAGATTTCGCAAGGCAAGGACCTTTGCAATAGCACCTGGAGCCAGAACCCAGAAATGTGCTCT 283  
 Db 867 -----LysGlyCysGlnAspLe-AsnGluCysAlaGlnProGlyLeuCysGly 882  
 QY 284 GAGAACGATCTTGTGATCTGACGCTGCTGCTTTTTCAGTCGCTGTTGCTGATGGT 343  
 Db 883 SerHisGlyGluCysLeuAsnThr---GlnGlySerPheHisCysValCysGluGlnGly 901  
 QY 344 TTC----- 346  
 Db 902 PheSerIleSerAlaAspGlyArgThrCysGluAspIleAspGluCysValAsnAsnThr 921  
 QY 347 -----CATGATACAACTGTATGAGGAGGCTCATTTTCACGTATGTTTC 394  
 Db 922 ValCysAspSerHisGlyPheCysAspAsnThrAlaGlySer-PheArgCysLeuCysTy 941  
 QY 395 TTTGGATCTGGGATCCA 413  
 Db 941 rGlnGlyPheGlnAlaPro 947  
 RESULT 13  
 ID LTBL RAT STANDARD; PRT; 1712 AA.  
 AC Q00918;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Latent transforming growth factor beta binding protein 1 precursor  
 DE (LTBP-1) (Transforming growth factor beta-1 binding protein 1) (TGF-  
 DE beta1-BP-1) (Transforming growth factor beta-1 masking protein, large  
 DE subunit).  
 CN LTBP1.  
 OS Rattus norvegicus (Rat).



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RA MEDLINE=91062373; PubMed=2247454;  
RA Tsuji T., Okada F., Yamaguchi K., Nakamura T.;  
RT "Molecular cloning of the large subunit of transforming growth factor  
RT type beta masking protein and expression of the mRNA in various rat  
RT tissues.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:8835-8839(1990).  
CC -!- SUBUNIT: The large latent complex of TGF-beta1 from platelets is  
CC composed of the TGF-beta1 molecule noncovalently associated with  
CC a masking protein consisting of a disulfide-bonded complex of a  
CC dimer of the N-terminal propeptide of the TGF-beta1 precursor and  
CC a third component denoted TGF-beta1-BP (or MP large subunit).  
CC TGF-beta1-BP does not bind directly to active TGF-beta1.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Contains 18 EGF-like domains.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M55431; AAA42235.1; -;  
DR FIR; A38261; A38261.  
DR HSP; P16109; LFSD.  
DR InterPro; IPR000152; Asx\_hydroxyl\_8.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR002212; Fibri1-associ.  
DR Pfam; PF00008; EGF; 16.  
DR Pfam; PF00683; TB; 4.  
DR SMART; SM00179; EGF\_CA; 13.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 13.  
DR PROSITE; PS00022; EGF\_1; 2.  
DR PROSITE; PS01196; EGF\_2; 10.  
DR PROSITE; PS00026; EGF\_3; 14.  
DR PROSITE; PS01187; EGF\_CA; 15.  
KW Growth factor binding; Repeat; EGF-like domain; Hydroxylation; Signal.  
FT SIGNAL 1 20 POTENTIAL.  
FT PROPEP 21 736 POTENTIAL.  
FT CHAIN 737 1577 LATENT TRANSFORMING GROWTH FACTOR BETA  
FT BINDING PROTEIN 1.  
FT SITE 734 736 CLEAVAGE (POTENTIAL).  
FT SITE 1575 1577 CLEAVAGE (POTENTIAL).  
FT PROPEP 1578 1712 POTENTIAL.  
FT DOMAIN 181 213 EGF-LIKE 1.  
FT DOMAIN 391 423 EGF-LIKE 2.  
FT REPEAT 551 604 INTERNAL REPEAT 1.  
FT DOMAIN 618 658 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).  
FT REPEAT 671 721 INTERNAL REPEAT 2.  
FT DOMAIN 865 906 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 907 948 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 949 989 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 990 1029 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 1030 1070 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 1071 1111 EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 1112 1152 EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 1153 1193 EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 1194 1235 EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 1236 1277 EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 1278 1320 EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).  
FT REPEAT 1340 1392 INTERNAL REPEAT 3.  
FT DOMAIN 1415 1457 EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 1458 1498 EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL).  
FT REPEAT 1517 1568 INTERNAL REPEAT 4.  
FT DOMAIN 1612 1652 EGF-LIKE 17.  
FT DOMAIN 1653 1697 EGF-LIKE 18, CALCIUM-BINDING (POTENTIAL).

FT DISULFID 185 195 BY SIMILARITY.  
FT DISULFID 189 201 BY SIMILARITY.  
FT DISULFID 203 212 BY SIMILARITY.  
FT DISULFID 395 405 BY SIMILARITY.  
FT DISULFID 399 411 BY SIMILARITY.  
FT DISULFID 413 422 BY SIMILARITY.  
FT DISULFID 622 633 BY SIMILARITY.  
FT DISULFID 628 642 BY SIMILARITY.  
FT DISULFID 644 657 BY SIMILARITY.  
FT DISULFID 869 881 BY SIMILARITY.  
FT DISULFID 876 890 BY SIMILARITY.  
FT DISULFID 892 905 BY SIMILARITY.  
FT DISULFID 911 923 BY SIMILARITY.  
FT DISULFID 918 932 BY SIMILARITY.  
FT DISULFID 934 947 BY SIMILARITY.  
FT DISULFID 953 964 BY SIMILARITY.  
FT DISULFID 959 973 BY SIMILARITY.  
FT DISULFID 976 988 BY SIMILARITY.  
FT DISULFID 994 1005 BY SIMILARITY.  
FT DISULFID 1000 1014 BY SIMILARITY.  
FT DISULFID 1017 1028 BY SIMILARITY.  
FT DISULFID 1034 1045 BY SIMILARITY.  
FT DISULFID 1040 1054 BY SIMILARITY.  
FT DISULFID 1056 1069 BY SIMILARITY.  
FT DISULFID 1075 1086 BY SIMILARITY.  
FT DISULFID 1081 1095 BY SIMILARITY.  
FT DISULFID 1097 1110 BY SIMILARITY.  
FT DISULFID 1116 1127 BY SIMILARITY.  
FT DISULFID 1122 1136 BY SIMILARITY.  
FT DISULFID 1138 1151 BY SIMILARITY.  
FT DISULFID 1157 1169 BY SIMILARITY.  
FT DISULFID 1164 1178 BY SIMILARITY.  
FT DISULFID 1180 1192 BY SIMILARITY.  
FT DISULFID 1198 1210 BY SIMILARITY.  
FT DISULFID 1204 1219 BY SIMILARITY.  
FT DISULFID 1221 1234 BY SIMILARITY.  
FT DISULFID 1240 1252 BY SIMILARITY.  
FT DISULFID 1246 1261 BY SIMILARITY.  
FT DISULFID 1263 1276 BY SIMILARITY.  
FT DISULFID 1282 1294 BY SIMILARITY.  
FT DISULFID 1289 1303 BY SIMILARITY.  
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FT DISULFID 1468 1482 BY SIMILARITY.  
FT DISULFID 1484 1497 BY SIMILARITY.  
FT DISULFID 1616 1627 BY SIMILARITY.  
FT DISULFID 1622 1636 BY SIMILARITY.  
FT DISULFID 1638 1651 BY SIMILARITY.  
FT DISULFID 1657 1672 BY SIMILARITY.  
FT DISULFID 1667 1681 BY SIMILARITY.  
FT DISULFID 1683 1696 BY SIMILARITY.  
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 370 370 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 416 416 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 612 612 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 1042 1042 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 1242 1242 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 1357 1357 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 1712 AA; 186598 MW; 650BCBA691FD134 CRC64;

Alignment Scores:  
Pred. No.: 0.038 Length: 1712  
Score: 98.50 Matches: 30  
Percent Similarity: 34.58% Conservative: 7  
Best Local Similarity: 28.04% Mismatches: 34  
Query Match: 11.09% Indels: 36  
DB: 1 Gaps: 4

US-09-773-476-294 (1-489) x LTBI\_RAT (1-1712)





Phan H., Velasco N., Ganes J., Danganan L., Poundstone P.,  
 Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T.,  
 Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,  
 Bruce R., Thomas P., Quan G., Krommiller B., Arellano A.,  
 Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S.,  
 Carrano A.V.;  
 "Sequence analysis of an 1.5 Mb olfactory receptor (OLFR) cluster in  
 19p13.1";  
 Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 [4]  
 VARIANTS CADASIL TIR-49; CYS-71; CYS-90; CYS-110; CYS-133; CYS-141;  
 ARG-146; CYS-153; CYS-169; CYS-171; CYS-182; ARG-185; SER-212;  
 GLY-222; TYR-224; CYS-258; TYR-542; CYS-558; CYS-578; CYS-728;  
 CYS-985; CYS-1006; CYS-1031; CYS-1231 AND ARG-1261, AND VARIANTS  
 ARG-170; LEU-496; GLN-1133; MET-1183 AND ALA-2223.  
 MEDLINE=98049753; PubMed=938939;  
 Joutel A., Vahedi K., Corpechot C., Troesch A., Chabriat H.,  
 Vayssiere C., Cruaud C., Maciazek J., Weissenbach J., Bousser M.-G.,  
 Bach J.-F., Tournier-Lasserre E.;  
 "Strong clustering and stereotyped nature of Notch3 mutations in  
 CADASIL patients";  
 Lancet 350:1511-1515(1997).  
 [5]  
 VARIANTS CADASIL 114-GLY-PRO-120 DEL.  
 MEDLINE=20264473; PubMed=10802807;  
 Joutel A., Chabriat H., Vahedi K., Domenga V., Vayssiere C.,  
 Ruchoux M.M., Lucas C., Leys D., Bousser M.-G., Tournier-Lasserre E.;  
 "Splice site mutation causing a seven amino acid Notch3 in-frame  
 deletion in CADASIL";  
 Neurology 54:1874-1875(2000).  
 [6]  
 IDENTIFICATION OF LIGANDS.  
 MEDLINE=99180765; PubMed=10079256;  
 Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,  
 Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;  
 "Human ligands of the Notch receptor";  
 Am. J. Pathol. 154:785-794(1999).  
 -1- FUNCTION: Functions as a receptor for membrane-bound ligands  
 Jagged1, Jagged2 and Delta1 to regulate cell-fate determination.  
 Upon ligand activation through the released notch intracellular  
 domain (NICD) it forms a transcriptional activator complex with  
 RBP-J kappa and activates genes of the enhancer of split locus.  
 Affects the implementation of differentiation, proliferation and  
 apoptotic programs (By similarity).  
 -1- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-  
 terminal fragment N(EC) which are probably linked by disulfide  
 bonds (By similarity).  
 -1- SUBCELLULAR LOCATION: Type I membrane protein. Following  
 proteolytical processing NICD is translocated to the nucleus.  
 -1- TISSUE SPECIFICITY: Ubiquitously expressed in fetal and adult  
 tissues.  
 -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form  
 which is proteolytically cleaved by a furin-like convertase in the  
 trans-Golgi network before it reaches the plasma membrane to yield  
 an active, ligand-accessible form. Cleavage results in a C-  
 terminal fragment N(TM) and a N-terminal fragment N(EC). Following  
 ligand binding, it is cleaved by TNF-alpha converting enzyme  
 (TACE) to yield a membrane-associated intermediate fragment called  
 notch extracellular truncation (NEXT). This fragment is then  
 cleaved by presenilin dependent gamma-secretase to release a  
 notch-derived peptide containing the intracellular domain (NICD)  
 from the membrane (By similarity).  
 -1- PFM: Phosphorylated (By similarity).  
 -1- DISEASE: Defects in NOTCH3 are associated with cerebral autosomal  
 dominant arteriopathy with subcortical infarcts and  
 leukoencephalopathy (CADASIL) [MIM:123310]. CADASIL causes a type  
 of stroke and dementia of which key features include recurrent  
 subcortical ischemic events and vascular dementia.  
 -1- SIMILARITY: Belongs to the NOTCH family.  
 -1- SIMILARITY: Contains 34 EGF-like domains.  
 -1- SIMILARITY: Contains 3 Lin/Notch repeats.  
 -1- SIMILARITY: Contains 5 ANK repeats.

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 EMBL; J97669; RAB91371.1; -;  
 EMBL; AF058900; AAC14346.1; -;  
 EMBL; AF058881; AAC14346.1; JOINED.  
 EMBL; AF058882; AAC14346.1; JOINED.  
 EMBL; AF058883; AAC14346.1; JOINED.  
 EMBL; AF058884; AAC14346.1; JOINED.  
 EMBL; AF058885; AAC14346.1; JOINED.  
 EMBL; AF058886; AAC14346.1; JOINED.  
 EMBL; AF058887; AAC14346.1; JOINED.  
 EMBL; AF058888; AAC14346.1; JOINED.  
 EMBL; AF058889; AAC14346.1; JOINED.  
 EMBL; AF058890; AAC14346.1; JOINED.  
 EMBL; AF058891; AAC14346.1; JOINED.  
 EMBL; AF058892; AAC14346.1; JOINED.  
 EMBL; AF058893; AAC14346.1; JOINED.  
 EMBL; AF058894; AAC14346.1; JOINED.  
 EMBL; AF058895; AAC14346.1; JOINED.  
 EMBL; AF058896; AAC14346.1; JOINED.  
 EMBL; AF058897; AAC14346.1; JOINED.  
 EMBL; AF058898; AAC14346.1; JOINED.  
 EMBL; AF058899; AAC14346.1; JOINED.  
 EMBL; AC004257; AAC04897.1; -;  
 EMBL; AC004563; AAC15789.1; ALT\_INIT.  
 FIRM; S78549; S78549.  
 HSP; P00740; IEDM.  
 Genew; HGNC:7883; NOTCH3.  
 MIM; 600276; -;  
 MIM; 125310; -;  
 InterPro; IPR002110; ANK.  
 InterPro; IPR000152; Asx\_hydroxyl\_S.  
 InterPro; IPR000742; EGF\_2.  
 InterPro; IPR001881; EGF\_Ca.  
 InterPro; IPR001438; EGF\_II.  
 InterPro; IPR006209; EGF\_like.  
 InterPro; IPR002049; Laminin\_EGF.  
 InterPro; IPR008297; Notch.  
 InterPro; IPR000800; Notch\_dom.  
 Pfam; PF00023; ank; 6.  
 Pfam; PF00008; EGF; 34.  
 Pfam; PF00066; notch; 3.  
 PIRSF; PIRSF002279; Notch; 1.  
 PRINTS; PR00010; EGF\_BLOOD.  
 PRINTS; PR00011; EGF\_LAMININ.  
 PRINTS; PR01452; NOTCH.  
 SMART; SM00248; ANK; 6.  
 SMART; SM00179; EGF\_CA; 19.  
 SMART; SM00004; NL; 3.  
 PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 PROSITE; PS50088; ANK\_REPEAT; 4.  
 PROSITE; PS00010; ASX\_HYDROXYL; 18.  
 PROSITE; PS00022; EGF\_1; 33.  
 PROSITE; PS01186; EGF\_2; 25.  
 PROSITE; PS50026; EGF\_3; 34.  
 PROSITE; PS01187; EGF\_CA; 16.  
 Receptor; Transcription regulation; Activator; Differentiation;  
 Developmental protein; Repeat; ANK repeat; EGF-like domain;  
 Transmembrane; Glycoprotein; Signal; Phosphorylation; Polymorphism;  
 Disease mutation.  
 SIGNAL 1 39 POTENTIAL.  
 CHAIN 40 2321 NOTCH EXTRACELLULAR TRUNCATION (BY  
 CHAIN 1629 2321 SIMILARITY).  
 CHAIN 1662 2321 NOTCH INTRACELLULAR DOMAIN (BY  
 SIMILARITY).  
 DOMAIN 40 1643 EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	1644	1664	POTENTIAL.	
FT	DOMAIN	1665	2321	CYTOPLASMIC (POTENTIAL).	
FT	DOMAIN	40	77	EGF-LIKE 1.	
FT	DOMAIN	78	118	EGF-LIKE 2.	
FT	DOMAIN	119	156	EGF-LIKE 3.	
FT	DOMAIN	158	195	EGF-LIKE 4.	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	197	235	EGF-LIKE 5.	
FT	DOMAIN	236	272	EGF-LIKE 6.	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	274	312	EGF-LIKE 7.	
FT	DOMAIN	314	350	EGF-LIKE 8.	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	351	389	EGF-LIKE 9.	
FT	DOMAIN	391	429	EGF-LIKE 10.	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	431	467	EGF-LIKE 11.	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	469	505	EGF-LIKE 12.	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	507	543	EGF-LIKE 13.	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	545	580	EGF-LIKE 14.	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	582	618	EGF-LIKE 15.	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	620	655	EGF-LIKE 16.	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	657	693	EGF-LIKE 17.	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	695	730	EGF-LIKE 18.	
FT	DOMAIN	734	770	EGF-LIKE 19.	
FT	DOMAIN	771	808	EGF-LIKE 20.	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	810	847	EGF-LIKE 21.	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	849	885	EGF-LIKE 22.	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	887	922	EGF-LIKE 23.	CALCIUM-BINDING (POTENTIAL).

  

Alignment Scores:			
Pred. No.:	0.0403	Length:	2321
Score:	98.50	Matches:	39
Percent Similarity:	30.56%	Conservative:	5
Best Local Similarity:	27.08%	Mismatches:	45
Query Match:	11.09%	Indels:	55
DB:	1	Gaps:	5

  

US-09-773-476-294 (1-489) x NTC3_HUMAN (1-2321)	
QY	52 TTTTACAGGTTTACTGCTATTATCATAGACCTTCAGGCAATCTCTCAAGATGATT 111
Db	461 PheThrGlyThrTy-Cys----- 466
QY	112 GGCCAAACACTTCGCTGGGTTTACTACGTGACACTCTGATACTACCAAGATGTTCC 171
Db	467 -----GluValAspIleAspGluCys-GluSerSerPr 477
QY	172 CTGTCTCGGAGTACTAATGCTGGGCAAGTTTACTTCTTCAAG----- 217
Db	477 OCysValasnGlyGlyValCysLysAspArgValasnGlyPheSerCysThrCysProSe 497
QY	218 -----GACAAAGCAGATTGCCAAGGCCAAGGACCTTTGCAATAGCAGCTGAAGGCC 270
Db	497 rGlyPheSerGlySerThrCysGlnLeuAspValAspGluCysAlaSerThr----- 514
QY	271 AGAAATGTCTCTGAGAACGAGTCTTGTCATCTGACGGTCTCGGCTTTTGAGTGGCT 330
Db	515 ----ProCys----ArgasnGlyAlaLysCysValAspGlnProAspGlyTyGluCysAr 532
QY	331 TTGTGCTGATGTTTCCATGATACAAGTGTATGAGGCAG----- 370
Db	532 gCysAladGluGlyPheGluGlyThrLeuCysAspArgAsnValAspAspCysSer-ProAs 552
QY	371 -----GGCTCATTTTCACTGCTTATGTTCTT 396
Db	552 pProCysHisHisGlyArgCysValAspGlyIleAlaSerPheSer-CysAlaCysAlap 572
QY	397 TGGGATTC 404
Db	572 roGlyTyAr 574



GenCore version 5.1.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 25, 2004, 09:10:13 ; Search time 44 Seconds  
(without alignments)  
7013.109 Million cell updates/sec

Title: US-09-773-476-294

Perfect score: 888

Sequence: 1 gactgagctagattcttcag.....tnatgagccacacaagactt 489

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2034082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame-n2p.model -DBV=xlp  
-Q/cg2.1/USPTC\_spool\_p/US09773476/runat\_25062004\_090846\_5828/app\_query.fasta\_1.647  
-DB=SPREMBL\_25 -QPMI=fastcan -SUFFIX=n2p.rspt -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORW=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09773476 @CGN 1.1.86 @runat\_25062004\_090846\_5828 -NCPV=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archheap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	807	90.9	162 11 Q810Q3	Q810q3 mus musculus

RESULT 1				
Q810Q3	Q810Q3	PRELIMINARY;	PRT;	162 AA.
ID	Q810Q3;			
AC	Q810Q3;			
DT	01-JUN-2003 (TrEMBLrel. 24, Created)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Similar to apoptosis related protein APR-3.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus			
OX	NCBI_TaxId=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RA	Strausberg R.;			
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC049637; AAA49637.1; -.			
DR	InterPro; IPR006209; EGF_like.			
DR	PROSITE; PS00022; EGF_1; 1.			
DR	PROSITE; PS01186; EGF_2; 1.			
SO	SEQUENCE 162 AA; 17519 MW; AD9498698BA1B71D CRC64;			

Alignment Scores: 4.5e-86 Length: 162  
Pred. No.: 162

2	796	89.6	223	11	Q9DD14	Q9dd14 mus musculus
3	690	77.7	171	4	Q9Y2R7	Q9y2r7 homo sapien
4	690	77.7	229	4	Q96FF6	Q96ff6 homo sapien
5	685	77.1	171	4	Q96XR2	Q96xr2 homo sapien
6	628	70.7	208	4	Q9Y5L7	Q9y5l7 homo sapien
7	109	12.3	382	11	Q8K1E3	Q8k1e3 mus musculus
8	108.5	12.2	713	5	Q962W9	Q962w9 podocoryne
9	105	11.8	2516	11	Q7TQ52	Q7tq52 mus musculus
10	105	11.8	2526	11	Q7TQ51	Q7tq51 mus musculus
11	105	11.8	2531	11	Q8K428	Q8k428 mus musculus
12	105	11.8	2531	11	Q7TQ50	Q7tq50 mus musculus
13	104.5	11.8	1065	11	Q810H2	Q810h2 mus musculus
14	102.5	11.5	2468	13	Q800E4	Q800e4 brachydanio
15	100.5	11.3	308	6	Q46370	Q46370 bos taurus
16	100.5	11.3	385	5	Q9U0E2	Q9u0e2 tribolium c
17	100.5	11.3	1511	4	Q754I2	Q754i2 homo sapien
18	100.5	11.3	1587	4	Q00508	Q00508 homo sapien
19	100.5	11.3	1722	5	Q19350	Q19350 caenorhabdi
20	99	11.1	2809	5	Q61230	Q61230 lytechinus
21	98	11.0	600	4	Q8N369	Q8n369 homo sapien
22	98	11.0	1282	4	Q8TER0	Q8ter0 homo sapien
23	97.5	11.0	191	13	Q9DED0	Q9ded0 gallus gall
24	97.5	11.0	1600	11	Q8K4G0	Q8k4g0 mus musculus
25	97.5	11.0	1666	11	Q8K4G1	Q8k4g1 mus musculus
26	97.5	11.0	2653	5	Q25253	Q25253 lucilia cup
27	97	10.9	420	5	Q8I499	Q8i499 cupiennius
28	97	10.9	1764	11	Q35806	Q35806 rattus norv
29	95.5	10.8	1515	13	Q9DE37	Q9de37 brachydanio
30	95	10.7	383	4	Q96DW5	Q96dw5 homo sapien
31	95	10.7	383	4	Q969T6	Q969t6 homo sapien
32	95	10.7	616	5	Q20852	Q20852 caenorhabdi
33	94.5	10.6	674	5	Q8T4N9	Q8t4n9 strongyloce
34	94.5	10.6	2524	5	Q9GPA5	Q9gpa5 brachiosteo
35	94	10.6	2352	5	Q61240	Q61240 halocynthia
36	94	10.6	3857	11	Q88840	Q88840 mus musculus
37	93.5	10.5	778	13	Q91BG4	Q91bg4 xenopus lae
38	93.5	10.5	794	5	Q8T4P0	Q8t4p0 lytechinus
39	93.5	10.5	1208	11	Q80YA8	Q80ya8 mus musculus
40	93.5	10.5	1799	11	Q8ROY0	Q8roy0 mus musculus
41	93.5	10.5	2531	5	Q16004	Q16004 lytechinus
42	92.5	10.4	2906	11	Q9WUH9	Q9wuh9 rattus norv
43	92	10.4	338	5	Q61126	Q61126 cryptospori
44	92	10.4	338	5	Q7Y160	Q7y160 cryptospori
45	92	10.4	614	5	Q86PP7	Q86pp7 cryptospori

Score: 807.00 Matches: 153  
Percent Similarity: 98.71% Conservative: 0  
Best Local Similarity: 98.71% Mismatches: 2  
Query Match: 90.88% Indels: 1  
DB: 11 Gaps: 0

US-09-773-476-294 (1-489) x Q810Q3 (1-162)

QY 6 AGGCTAGCTTTCAGACTGCTCCCTCAG-GATCCTGGTCCAAACTTTTACAGGCTTAT 64  
Db 7 ArgLeuAspLeuGlnAsnCysSerLeuLeuAspProGlyProAsnPheLeuGlnAlaTyr 26  
QY 65 ACTGCTATTATCATAGACTTCAGGCTTCAGGCTTCCTCAGGATGATTTGGCCACACCTTC 124  
Db 27 ThrAlaIleIleAspLeuGlnAlaAsnProLeuLysAspAspLeuAlaAsnThrPhe 46  
QY 125 CGTGGGTTTACTCAGCTGCAGACTCTCATACTACCAAGATGTTCCCTGCTCCTGGAGGT 184  
Db 47 ArgGlyPheThrGlnLeuGlnThrLeuLeuLeuProGlnAspValProCysProGlyGly 66  
QY 185 AGTAATCCCTGGGACAATGTTACTCTTTTCAAGACAAGCAGATTTGCCAAGGCAAGG 244  
Db 67 SerAsnAlaTrpAspAsnValThrSerPheLysAspLysGlnIleCysGlnGlyGlnArg 86  
QY 245 GACCTTTGCAATAGCACTGGAAGCCAGAAATGTGCTCAGAACGATCTTCTGCTGATCT 304  
Db 87 AspLeuCysAsnSerThrGlySerProGluMetCysProGluAsnGlySerCysAlaSer 106  
QY 305 GACGGTCTCTCTTTGCAAGTGGTGTGCTGATGTTTCCATGATGATCAAGTCTATG 364  
Db 107 AspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCysMet 126  
QY 365 AGGAGAGCTCATTTTCACTGCTTATGTTTCTTGGGATCTGGGATCCACCGCTAGCC 424  
Db 127 ArgGlnGlySerPheSerLeuLeuMetPhePheGlyLeuLeuGlySerThrThrLeuAla 146  
QY 425 ATCTNCTATTCTACTTTGGGAAACCCAGCGCGGAAAGCCAGGCT 469  
Db 147 IleSerIleLeuLeuTrpGlyThrGlnArgArgLysAlaLysAla 161

RESULT 2  
Q9DD14 PRELIMINARY; PRT; 223 AA.  
AC Q9DD14  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE 0610007C2IRik protein.  
GN APR3 OR 0610007C2IRIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Kidney;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant R.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schirf L.M., Staehli F., Suzuki R., Tonita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann J., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
RA Hayashizaki Y.,  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
DR EMBL; AK002276; BAB21981.1; -.  
DR MGD; MGI:1918918; Apr3  
DR InterPro; IPR006209; EGF-like.  
DR SMART; SM00181; EGF; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
KW EGF-like domain.  
SQ SEQUENCE 223 AA; 23867 MW; A85E3A03C7DD2C16 CRC64;  
Alignment Scores:  
Pred. No.: 9,47e-85 Length: 223  
Score: 796.00 Matches: 152  
Percent Similarity: 98.08% Conservative: 1  
Best Local Similarity: 97.44% Mismatches: 3  
Query Match: 89.64% Indels: 1  
DB: 11 Gaps: 0

US-09-773-476-294 (1-489) x Q9DD14 (1-223)

QY 3 CTGAGCTAGATCTTCAGAACTGTTCCCTCAG-GATCCTGGTCCAAACTTTTACAGGCT 61  
Db 67 LeuGlyLeuAsnLeuGlnAsnCysSerLeuLysAspProGlyProAsnPheLeuGlnAla 86  
QY 62 TATACCTGATATATCATAGACTTCAGGCAAAATCCTCTCAAGGATGATTTGGCCAAAC 121  
Db 87 TyrThrAlaIleIleAspLeuGlnAlaAsnProLeuLysAspAspLeuAlaAsnThr 106  
QY 122 TTCCTGGGTTTACTCAGCTGCAGACTCTGATCTACCAAGATGTTCCCTGCTCCTGGA 181  
Db 107 PheArgGlyPheThrGlnLeuGlnThrLeuLeuLeuProGlnAspValProCysProGly 126  
QY 182 GGTAGTAACTGCTGGGACAATGTTACTTCTTCAAGGACAAGCAGATTTCCAAAGGCCAA 241  
Db 127 GlySerAsnAlaTrpAspAsnValThrSerPheLysAspLysGlnIleCysGlnGlyGln 146  
QY 242 AGGACCTTTCCAACTAGCACTGGAAGCCAGAAATGTCTCAGAACGATCTTGTGCA 301  
Db 147 ArgAspLeuCysAsnSerThrGlySerProGluMetCysProGluAsnGlySerCysAla 166  
QY 302 TCTGACGGTCTCTGCTTCTTTCAGTGGGTTTGTCTGATGTTTCCATGGATCAAGTGT 361  
Db 167 SerAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys 186  
QY 362 ARGAGGAGGGCTCATTTTCACTGCTTATGTTCTTTGGGATCTGGGATCCACACGCTA 421  
Db 187 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyLeuLeuGlySerThrThrLeu 206  
QY 422 GCCATCTNCTACTTCTACTTTGGGAAACCCAGCGCGGAAAGCCAGGCT 469  
Db 207 AlaIleSerIleLeuLeuTrpGlyThrGlnArgArgLysAlaLysAla 222

RESULT 3  
Q9Y2R7 PRELIMINARY; PRT; 171 AA.  
AC Q9Y2R7  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-NOV-2003 (TrEMBLrel. 23, Last annotation update)  
DE HSPC013 (Apoptosis related protein APR-3).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
SEQUENCE FROM N.A.  
RP MEDLINE=20499367; PubMed=11042152;  
RX Zhang Q.H., Ye M., Wu X.Y., Ren S.X., Zhao M., Zhao C.J., Fu G.,  
RA Shen Y., Fan H.Y., Lu G., Zhong M., Xu X.R., Han Z.G., Zhang J.W.,



RA Tao J., Huang Q.H., Zhou J., Hu G.X., Gu J., Chen S.J., Chen Z.;  
RT "Cloning and functional analysis of cDNAs with open reading frames for  
ET 300 previously undefined genes expressed in CD34+ hematopoietic  
stem/progenitor cells";  
RL Genome Res. 10:1546-1560(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF077037; AAD27770.1; -  
DR EMBL; BC035850; AAH35850.1; -  
DR EMBL; BC035850; AAH35850.1; -  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR006210; IEGF.  
DR SMART; SM00181; EGF; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
KW EGF-like domain.  
SQ SEQUENCE 171 AA; 18597 MW; 91A42CD2B2CB0883 CRC64;  
  
Alignment Scores:  
Pred. No.: 2,876-72 Length: 171  
Score: 690.00 Matches: 128  
Percent Similarity: 89.68% Conservative: 11  
Best Local Similarity: 82.58% Mismatches: 16  
Query Match: 77.70% Indels: 1  
DB: 4 Gaps: 0  
  
US-09-773-476-294 (1-489) x Q9Y2R7 (1-171)  
  
QY 3 CTGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCCTGGTCCAACTTTTACAGGCT 61  
Db 15 LeuGlyLeuAspLeuGlnAsnProGlyProAsnPheHisGlnAla 34  
  
QY 62 TATACCTGCTATTATCATAGACCTTCAGCAATCTCTCAAGGATGATTGGCCAAACACC 121  
Db 35 HisThrThrValIleLeuAspLeuGlnAsnProLeuLysGlyAspLeuAlaAsnThr 54  
  
QY 122 TTCCTGGGTTTACTCAGCTGAGACTGTGATCTACACAGATGTTCCCTGCTCTGGA 181  
Db 55 PheArgGlyPheThrGlnLeuGlnThrLeuLeuProGlnHisValAsnProGly 74  
  
QY 182 GGTAGTAATCTGGGCAATGTTACTTCTTCAAGGCAACAGCAGATTGGCCAGGCAA 241  
Db 75 GlyIleAsnAlaTrpAsnThrIleThrSerTyrlleAspAsnGlnIleCysGlnGlyGln 94  
  
QY 242 AGGACCTTTGCAATAGCACTGGAGCCGCAAAATGTGTCCTGAGAACGGATCTTGCA 301  
Db 95 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 114  
  
QY 302 TCTGACGGTCTGGTCTTTTTCAGTGGTGTGCTGATGTTTCCATGGATACAGTGT 361  
Db 115 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrlLysCys 134  
  
QY 362 ATGAGGAGGGCTCATTTTCACTGCTTATGTTCTTTGGGATCTGGGATCCACACGCTA 421  
Db 135 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 154  
  
QY 422 GCCATCTNCAATTTACTTTGGGAAACCCAGCCCGGAAAGCCCAAG 466  
Db 155 SerValSerIleLeuLeuTrpAlaThrGlnArgLysAlaLys 169  
  
RESULT 4  
Q96FF6 PRELIMINARY; PRT; 229 AA.  
AC Q96FF6  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
  
RA Yang Y.C., Chen S.Y., Chang M.S.;  
RP SEQUENCE FROM N.A.  
RN [1]  
RS NCBI\_TaxID=9606;  
RC TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC011006; AAH11006.1; -  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR006210; IEGF.  
DR SMART; SM00181; EGF; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
KW Hypothetical protein; EGF-like domain.  
SQ SEQUENCE 229 AA; 24688 MW; F2C63F934A47ED33 CRC64;  
  
Alignment Scores:  
Pred. No.: 3,036-72 Length: 229  
Score: 690.00 Matches: 128  
Percent Similarity: 89.68% Conservative: 11  
Best Local Similarity: 82.58% Mismatches: 16  
Query Match: 77.70% Indels: 1  
DB: 4 Gaps: 0  
  
US-09-773-476-294 (1-489) x Q96FF6 (1-229)  
  
QY 3 CTGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCCTGGTCCAACTTTTACAGGCT 61  
Db 73 LeuGlyLeuAspLeuGlnAsnProGlyProAsnPheHisGlnAla 92  
  
QY 62 TATACCTGCTATTATCATAGACCTTCAGCAATCTCTCAAGGATGATTGGCCAAACACC 121  
Db 93 HisThrThrValIleLeuAspLeuGlnAsnProLeuLysGlyAspLeuAlaAsnThr 112  
  
QY 122 TTCCTGGGTTTACTCAGCTGAGACTGTGATCTACACAGATGTTCCCTGCTCTGGA 181  
Db 113 PheArgGlyPheThrGlnLeuGlnThrLeuLeuProGlnHisValAsnProGly 132  
  
QY 182 GGTAGTAATCTGGGCAATGTTACTTCTTCAAGGCAACAGCAGATTGGCCAGGCAA 241  
Db 133 GlyIleAsnAlaTrpAsnThrIleThrSerTyrlleAspAsnGlnIleCysGlnGlyGln 152  
  
QY 242 AGGACCTTTGCAATAGCACTGGAGCCGCAAAATGTGTCCTGAGAACGGATCTTGCA 301  
Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172  
  
QY 302 TCTGACGGTCTGGTCTTTTTCAGTGGTGTGCTGATGTTTCCATGGATACAGTGT 361  
Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrlLysCys 192  
  
QY 362 ATGAGGAGGGCTCATTTTCACTGCTTATGTTCTTTGGGATCTGGGATCCACACGCTA 421  
Db 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212  
  
QY 422 GCCATCTNCAATTTACTTTGGGAAACCCAGCCCGGAAAGCCCAAG 466  
Db 213 SerValSerIleLeuLeuTrpAlaThrGlnArgLysAlaLys 227  
  
RESULT 5  
Q96RT2 PRELIMINARY; PRT; 171 AA.  
AC Q96RT2  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE P18 protein.  
GN P18.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yang Y.C., Chen S.Y., Chang M.S.;

RT "Cloning and characterization of p18";  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF275744; AAR69412.1; -.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR006210; IEGF.  
 DR SMART; SM00181; EGF; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 KW EGF-like domain.  
 SQ SEQUENCE 171 AA; 18567 MW; 81A52CD2B2CE0883 CRC64;

Alignment Scores:  
 Pred. No.: 6,13e-65 Length: 208  
 Score: 628.00 Matches: 122  
 Percent Similarity: 82.82% Conservative: 13  
 Best Local Similarity: 74.85% Mismatches: 28  
 Query Match: 70.72% Indels: 2  
 DB: 4 Gaps: 0

US-09-773-476-294 (1-489) x Q9Y5L7 (1-208)

QY 3 CTGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCTGCTGCTCAAACTTTTACAGGCT 61  
 DB LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 58  
 QY 62 TATACCTGCTATATCATAGACCTTCAGGCAATCTCTCAAGGATGATTTGGCCAAACACC 121  
 DB HisThrThrValIleLeuAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 78  
 QY 122 TTCGCTGGGTTTACTCAGCTCAGACTCTGATATACACAAAGATGTTCCCTGCTCTGGA 181  
 DB PheArgGlyPheThrGlnLeuGlnThrLeuLeuProGlnHisValAsnCysProGly 98  
 QY 182 GSTAGTAACTGCTCGGCAATGTTACTTCTTCAAGGACAGAGATTTGCCAAGGCA 241  
 DB GlyLeuAsnAlaTrpAsnThrIleThrSerTyrIleAspAsnGlnIleCysGlnGln 118  
 QY 242 AGGACCTTTTCAATAGACCTGGAAGCCAGAAATGTCTCTGAGAACGGATCTTGTGCA 301  
 DB LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 138  
 QY 302 TCTGACGCTCTGCTCTTTCAGTGGTGTGTCTGATGTTCCATGGATA-CRAAGTG 360  
 DB ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyIleGlnVal 158  
 QY 361 TATCAGGCGAGGCTCATTTTTCATCTGCTTATGTTCTTGGGATCTCGGATCCACAGCT 420  
 DB TyrAlaProGlyLeuValLeuThrAlaTyrValLeuArgAspSerGlySerHisHisser 178  
 QY 421 AGCATCTNCATTTCTACTTTGGGAAACCCAGCGCCGGAAGCCAGGCTTNATGAGCAC 480  
 DB IleArgLeuHisSerAlaLeuGlyGlyProAlaProLysSerGlnAspPheMetAsnTyr 198  
 QY 481 ACAAGACTT 489  
 DB 199 IleglyLeu 201

RESULT 7

Q8K1E3 PRELIMINARY; PRT; 382 AA.  
 AC Q8K1E3;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Similar to hypothetical protein MGC2487.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP TISSUE=Salivary gland;  
 RC SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC019431; AAH19431.1; -.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF-Ca.  
 DR InterPro; IPR001438; EGF-II.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR002049; Laminin\_EGF.

RT "Cloning and characterization of p18";  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF275744; AAR69412.1; -.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR006210; IEGF.  
 DR SMART; SM00181; EGF; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 KW EGF-like domain.  
 SQ SEQUENCE 171 AA; 18567 MW; 81A52CD2B2CE0883 CRC64;

Alignment Scores:  
 Pred. No.: 1.12e-71 Length: 171  
 Score: 685.00 Matches: 127  
 Percent Similarity: 89.03% Conservative: 11  
 Best Local Similarity: 81.94% Mismatches: 17  
 Query Match: 77.14% Indels: 1  
 DB: 4 Gaps: 0

US-09-773-476-294 (1-489) x Q96RT2 (1-171)

QY 3 CTGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCTGCTGCTCAAACTTTTACAGGCT 61  
 DB LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 34  
 QY 62 TATACCTGCTATATCATAGACCTTCAGGCAATCTCTCAAGGATGATTTGGCCAAACACC 121  
 DB HisThrThrValIleLeuAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 54  
 QY 122 TTCGCTGGGTTTACTCAGCTCAGACTCTGATATACACAAAGATGTTCCCTGCTCTGGA 181  
 DB PheArgGlyPheThrGlnLeuGlnThrLeuLeuProGlnHisValAsnCysProGly 74  
 QY 182 GSTAGTAACTGCTCGGCAATGTTACTTCTTCAAGGACAGAGATTTGCCAAGGCA 241  
 DB GlyLeuAsnAlaTrpAsnThrIleThrSerTyrIleAspAsnGlnIleCysGlnGln 94  
 QY 242 AGGACCTTTTCAATAGACCTGGAAGCCAGAAATGTCTCTGAGAACGGATCTTGTGCA 301  
 DB LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 114  
 QY 302 TCTGACGCTCTGCTCTTTCAGTGGTGTGTCTGATGTTCCATGGATCAAGTGT 361  
 DB ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys 134  
 QY 362 ATGAGGCGAGGCTCATTTTTCATCTGCTTATGTTCTTGGGATCTCGGATCCACAGCTA 421  
 DB MetArgGlySerPheSerLeuLeuMetPheGlyLeuGlyAlaThrThrLeu 154  
 QY 422 GCCATCTNCATTTCTACTTTGGGAAACCCAGCGCCGGAAGCCCAAG 466  
 DB 155 SerValSerIleLeuLeuTrpAlaAlaGlnArgLysAlaLys 169

RESULT 6

Q9Y5L7 PRELIMINARY; PRT; 208 AA.  
 AC Q9Y5L7;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Apoptosis related protein APR-3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhu F., Yan W., Chai Y.B., Shao C., Peng W.D., Yang A.G., Wang C.J.,  
 RA Zhao Z.L.;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF144055; AAD31317.2; -.  
 SQ SEQUENCE 208 AA; 22687 MW; CD4C5723C62CAF6F CRC64;



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DB:              11          Gaps:      8

US-09-773-476-294 (1-489) x Q7TQ51 (1-2516)
QY 53 TTACAGGCTTATACTGCT-----ATTATCATAGACCTTCAG-----GCATAATCCT 97
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 426 LeuGlnGlyTyrThrGlyProArgCysGluIleAspValAsnGluCysIleSerAsnPro 445
QY 98 CTCAGAGATGATTGGCCACACCTTCCTGGGGTTTACTCAGCTGCAGACTCTGTACTACTA 157
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 446 CysGlnAsnAsp---AlaThrCysLeuAspGlnIleGlyGluPheGlnCysIleCysMet 464
QY 158 CCA-----CAAGATGTTCCCTGT 175
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 465 ProGlyTyrGluGlyValTyrCysGluIleAsnThrAspGluCysAlaSerSerProCys 484
QY 176 CCTGGAGTAGTAATGCTGGGACAATGTTACTTCTTCTTCAAG----- 217
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 485 LeuHisAsnGlyHisCysMetAspLysIleAsnGluPheGlnCysGlnCysProLysGly 504
QY 218 ---GACAGCAGATTTCCAGGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG 274
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 505 PheAsnGlyHisLeuCysGlnTyrAspValAspGluCysAlaSerThr----- 520
QY 275 ATGTGCTCTGAGAACGATCTTGTGCATCTGACGGTCTCTGCTTTTGCAGTGCCTTGT 334
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 521 ProCys---LysAsnGlyAlaLysCysLeuAspGlyProAsnThrTyrThrCysValCys 539
QY 335 GCTGATGTTTCCATGATACAAAGTGT----- 361
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 540 ThrGluGlyTyrThrGlyHisCysGluValAspIleAspGluCysAspProAspPro 559
QY 362 -----ATGAGCAGGGCTCATTTTCTGCTTATGTTCTTTGGG 400
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 560 CysHisTyrGlySerCysLysAsp-GlyValAlaThrPheThrCysLeuCysGlnProGl 579
QY 401 ATTC 404
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 579 YTYR 580

RESULT 10
Q7TQ51 PRELIMINARY; PRT; 2526 AA.
ID Q7TQ51 AC Q7TQ51;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Transmembrane receptor Notch1 D.
GN NOTCH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C.B-17; TISSUE=Thymus;
RA Tsuji H., Ishii-Obata H., Ukai H., Katsube T., Ogii T.;
RT "Radiation-induced deletions in the 5' end region of Notch1 lead to
RT the formation of truncated proteins and are involved in the
RT development of mouse thymic lymphomas.";
RL Carcinogenesis 24:1-12(2003).
DR EMBL; AB100603; BAC77039.1; -.
KW Receptor; Transmembrane.
SQ SEQUENCE 2526 AA; 270583 MW; 017563FCE9703264 CRC64;

Alignment Scores:
Pred. No.: 0.0048 Length: 2526
Score: 105.00 Matches: 41
Percent Similarity: 35.80% Conservatives: 17
Best Local Similarity: 25.31% Mismatches: 53
Query Match: 11.82% Indels: 8
DB: 11 Gaps: 8

```

```

US-09-773-476-294 (1-489) x Q7TQ51 (1-2526)
QY 53 TTACAGGCTTATACTGCT-----ATTATCATAGACCTTCAG-----GCAATATCCT 97
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 436 LeuGlnGlyTyrThrGlyProArgCysGluIleAspValAsnGluCysIleSerAsnPro 455
QY 98 CTCAGAGATGATTGGCCACACCTTCCTGGGGTTTACTCAGCTGCAGACTCTGTACTACTA 157
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 456 CysGlnAsnAsp---AlaThrCysLeuAspGlnIleGlyGluPheGlnCysIleCysMet 474
QY 158 CCA-----CAAGATGTTCCCTGT 175
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 475 ProGlyTyrGluGlyValTyrCysGluIleAsnThrAspGluCysAlaSerSerProCys 494
QY 176 CCTGGAGTAGTAATGCTGGGACAATGTTACTTCTTCTTCAAG----- 217
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 495 LeuHisAsnGlyHisCysMetAspLysIleAsnGluPheGlnCysGlnCysProLysGly 514
QY 218 ---GACAGCAGATTTCCAGGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG 274
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 515 PheAsnGlyHisLeuCysGlnTyrAspValAspGluCysAlaSerThr----- 530
QY 275 ATGTGCTCTGAGAACGATCTTGTGCATCTGACGGTCTCTGCTTTTGCAGTGCCTTGT 334
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 531 ProCys---LysAsnGlyAlaLysCysLeuAspGlyProAsnThrTyrThrCysValCys 549
QY 335 GCTGATGTTTCCATGATACAAAGTGT----- 361
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 550 ThrGluGlyTyrThrGlyHisCysGluValAspIleAspGluCysAspProAspPro 569
QY 362 -----ATGAGCAGGGCTCATTTTCTGCTTATGTTCTTTGGG 400
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 570 CysHisTyrGlySerCysLysAsp-GlyValAlaThrPheThrCysLeuCysGlnProGl 589
QY 401 ATTC 404
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 589 YTYR 590

RESULT 11
Q8K428 PRELIMINARY; PRT; 2531 AA.
ID Q8K428 AC Q8K428;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Notch 1 protein.
GN NOTCH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Thymus;
RA MEDLINE=95044925; PubMed=7956822;
RA Nye J.S., Kopan R., Axel R.;
RT "An activated Notch suppresses neurogenesis and myogenesis but not
RT gliogenesis in mammalian cells.";
RL Development 120:2421-2430(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Thymus;
RX MEDLINE=22115993; PubMed=12123574;
RA Foltz D.R., Santiago M.C., Berechid B.E., Nye J.S.;
RT "Glycogen Synthase Kinase-3beta Modulates Notch Signaling and
RT Stability.";
RL Curr. Biol. 12:1006-1011(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Thymus;
RA Schellin K.A., Pauley A.M., Nye J.S.;
RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF508809; AAM28905.1; -.
DR

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DR MGD; MGI:97363; Notch1.  
DR GO; GO:0005515; P:protein binding; IPI.  
DR GO; GO:0030154; P:cell differentiation; IMP.  
DR GO; GO:0007386; P:compartment specification; IMP.  
DR GO; GO:0045944; P:positive regulation of transcription from P. . . ; IDA.  
DR InterPro; IPR002110; ANK.  
DR InterPro; IPR000152; Asx hydroxyl\_S.  
DR InterPro; IPR000742; EGF 2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001438; EGF-II.  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR002049; Laminin\_EGF.  
DR InterPro; IPR008297; Notch.  
DR InterPro; IPR000800; Notch\_dom.  
DR Pfam; PF00023; ank; 6.  
DR Pfam; PF00008; EGF; 36.  
DR Pfam; PF00066; notch; 3.  
DR PRINTS; PR00010; EGFELOOD.  
DR PRINTS; PR00011; EGFELAMIN.  
DR PRINTS; PR01452; NOTCH.  
DR SMART; SM00248; ANK; 6.  
DR SMART; SM00181; EGF; 37.  
DR SMART; SM00179; EGF\_CA; 35.  
DR SMART; SM00004; NL; 3.  
DR PROSITE; PS50088; ANK\_REPEAT; 4.  
DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 22.  
DR PROSITE; PS00022; EGF 1; 35.  
DR PROSITE; PS01186; EGF 2; 27.  
DR PROSITE; PS01187; EGF\_CA; 21.  
DR PIRSF; PIRSF002279; Notch; 1.  
KW ANK repeat; EGF-like domain; Repeat.  
SQ SEQUENCE 2531 AA; 270819 MW; 7DB7E0DEF799D999 CRC64;

Alignment Scores:  
Pred. No.: 0.0048 Length: 2531  
Score: 105.00 Matches: 41  
Percent Similarity: 35.80% Conservative: 17  
Best Local Similarity: 25.31% Mismatches: 53  
Query Match: 11.82% Indels: 51  
DB: 11 Gaps: 8

US-09-773-476-294 (1-489) x Q8K428 (1-2531)

QY 53 TTACAGGCTTATCTGCT-----ATTATCATAGACCTTCAG-----GCAAACTCT 97  
DB 441 LeuGlnGlyTyrThrGlyProArgCysGluLeuAspValAsnGluCysIleSerAsnPro 460  
QY 98 CTCAGAGGATGTTGGCCCAACACCTTCGCTGGGTTTACTAGCTGCAGACTCTGATCTA 157  
DB 461 CysGlnAsnAsp---AlaThrCysLeuAspGlnIleGlyGluPheGlnCysIleCysMet 479  
QY 158 CCA-----CAAGATGTTCCCTGT 175  
DB 480 ProGlyTyrGluGlyValTyrCysGluLeuAsnThrAspGluCysAlaSerSerProCys 499  
QY 176 CTGGAGGTAGTAATGCTGGGACAATGTTACTTCTTCAAG----- 217  
DB 500 LeuHisAsnGlyHisCysMetAspLysIleAsnGluPheGlnCysGlnCysProLysGly 519  
QY 218 ---GACAGCAGATTTGCCAAGGCGAAGGACCTTTGCAATAGCAGCTGGAAGCCAGAA 274  
DB 520 PheAsnGlyHisLeuCysGlnTyrAspValAspGluCysAlaSerThr----- 535  
QY 275 ATGTGCTCAGAACGAGTCTTGTCATCTGACGCTCGCTGCTTTTGCAGTGGCTTGT 334  
DB 536 ProCys---LysAsnGlyAlaLysCysLeuAspGlyProAsnThrTyrThrCysValCys 554  
QY 335 GCTGATGTTTCCATGATACAAAGTGT----- 361  
DB 555 ThrGluGlyTyrThrGlyThrHisCysGluValAspIleAspGluCysAspProAspPro 574  
QY 362 -----ATGAGCGAGGCTCATTTCACTGCTTATGTTCTTTGG 400

QY 362 -----ATGAGCGAGGCTCATTTCACTGCTTATGTTCTTTGG 400  
DB 575 CysHisTyrGlySerCysLysAsp-GlyValAlaThrPheThrCysLeuCysGlnProGl 594  
QY 401 ATTC 404  
DB 594 YTYR 595  
RESULT 12  
Q7TQ50 PRELIMINARY; PRT; 2531 AA.  
ID Q7TQ50  
AC Q7TQ50;  
DT 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Transmembrane receptor Notch1.  
GN NOTCH1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
CX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C.B-17; TISSUE=Thymus;  
RA Tsuji H., Ishii-Orba H., Ukai H., Katsube T., Ogizu T.;  
RT "Radiation-induced deletions in the 5' end region of Notch1 lead to  
RT the formation of truncated proteins and are involved in the  
RT development of mouse thymic lymphomas."  
RL Carcinogenesis 24:1-12(2003).  
DR EMBL; AB10603; BAC77040.1; -.  
KW Receptor; Transmembrane.  
SQ SEQUENCE 2531 AA; 270832 MW; 97C91F69BABF02BF CRC64;

Alignment Scores:  
Pred. No.: 0.0048 Length: 2531  
Score: 105.00 Matches: 41  
Percent Similarity: 35.80% Conservative: 17  
Best Local Similarity: 25.31% Mismatches: 53  
Query Match: 11.82% Indels: 51  
DB: 11 Gaps: 8

US-09-773-476-294 (1-489) x Q7TQ50 (1-2531)

QY 53 TTACAGGCTTATCTGCT-----ATTATCATAGACCTTCAG-----GCAAACTCT 97  
DB 441 LeuGlnGlyTyrThrGlyProArgCysGluLeuAspValAsnGluCysIleSerAsnPro 460  
QY 98 CTCAGAGGATGTTGGCCCAACACCTTCGCTGGGTTTACTAGCTGCAGACTCTGATCTA 157  
DB 461 CysGlnAsnAsp---AlaThrCysLeuAspGlnIleGlyGluPheGlnCysIleCysMet 479  
QY 158 CCA-----CAAGATGTTCCCTGT 175  
DB 480 ProGlyTyrGluGlyValTyrCysGluLeuAsnThrAspGluCysAlaSerSerProCys 499  
QY 176 CTGGAGGTAGTAATGCTGGGACAATGTTACTTCTTCAAG----- 217  
DB 500 LeuHisAsnGlyHisCysMetAspLysIleAsnGluPheGlnCysGlnCysProLysGly 519  
QY 218 ---GACAGCAGATTTGCCAAGGCGAAGGACCTTTGCAATAGCAGCTGGAAGCCAGAA 274  
DB 520 PheAsnGlyHisLeuCysGlnTyrAspValAspGluCysAlaSerThr----- 535  
QY 275 ATGTGCTCAGAACGAGTCTTGTCATCTGACGCTCGCTGCTTTTGCAGTGGCTTGT 334  
DB 536 ProCys---LysAsnGlyAlaLysCysLeuAspGlyProAsnThrTyrThrCysValCys 554  
QY 335 GCTGATGTTTCCATGATACAAAGTGT----- 361  
DB 555 ThrGluGlyTyrThrGlyThrHisCysGluValAspIleAspGluCysAspProAspPro 574  
QY 362 -----ATGAGCGAGGCTCATTTCACTGCTTATGTTCTTTGG 400

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Db 575 CysHisTyrGlySerCysLysAsp-GlyValAlaThrPheThrCysLeuCysGlnProgl 594
QY 401 ATTC 404
Db 594 YTYR 595
RESULT 13
ID Q810H2 PRELIMINARY; PRT; 1065 AA.
AC Q810H2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Secreted protein SST3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Ueno H.;
RT "A stromal cell-derived membrane protein that supports hematopoietic
stem cells.";
RL Nat. Immunol. 0:0-0(2003).
DR EMBL; AY169783; AAC41836.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR000152; ASX_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001886; Nidogen_ext.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00008; EGF; 13.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00084; sushi; 1.
DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00011; EGF_LAMININ.
DR SMART; SMC0032; CCP; 1.
DR SMART; SMC0181; EGF; 14.
DR SMART; SMC0179; EGF_CA; 13.
DR SMART; SMC0060; FN3; 1.
DR SMART; SMC0539; NIDO; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 6.
DR PROSITE; PS00022; EGF_1; 14.
DR PROSITE; PS01186; EGF_2; 13.
DR PROSITE; PS01187; EGF_CA; 3.
SQ SEQUENCE 1065 AA; 114283 MW; 899E199C51139D80 CRC64;

Alignment Scores:
Pred. No.: 0.00468 Length: 1065
Score: 104.50 Matches: 37
Percent Similarity: 29.86% Conservatives: 6
Best Local Similarity: 25.69% Mismatches: 33
Query Match: 11.77% Indels: 68
DB: 7 Gaps: 7

US-09-773-476-294 (1-489) x Q810H2 (1-1065)
QY 161 CAAGATGTCCTGCTCGAGTAGTAATGCTGGGCAATGTTACTTCTTCAGGAC 220
Db 796 GlnAlaGlnProCysArgAsnGlySerCysArgAspLeuProArgAlaPhe----- 813
QY 221 AAGCAGATTGGCAA-----GGGCAAAAGGAC 247
Db 814 -----IleCysGlnCysProGluGlyPheValGlyIleHisCysGluThrGluValAsp 831
QY 248 CTTTGAATAGCACTGGAAGCCAGAAATGTCCTGAGAACGGATCTTGTCATCTGAC 307

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Db 832 AlaCysAlaSer-----SerPro-----CysGlnHisGlyGlyArgCys---GluAsp 846
QY 308 GGTCTGGTCTTTTGCAGTGGCTTGTGCTGATGGTTTCCATGATACAAAGTGT----- 361
Db 847 GlyGlyGlyAlaTyrLeuCysValCysProGluGlyPhePheGlyTyrAsnCysGluThr 866
QY 362 -----ATGAGGCAG 370
Db 867 MetSerAspProCysPheSerSerProCysGlySerArgGlyTyrCysLeuAlaSerAsn 886
QY 371 GGCTCATTTTCACGTGCTATGTTCTTTGGGATTC----- 404
Db 887 GlySerHisSer-CysThrCysLysValGlyTyrThrGlyLysAspCysThrLysGluLe 906
QY 405 -----TG 406
Db 906 uLeuProProThrAlaLeuArgValGluArgValGluSerGlyValSerIleSerTr 926
QY 407 GGATCCACCA 416
Db 926 pSerProPro 929
RESULT 14
ID Q800E4 PRELIMINARY; PRT; 2468 AA.
AC Q800E4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Notch3.
GN NOTCH3.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim C.-H., Chitnis A.;
RT "Zebrafish Notch3 and Neural Plate Formation.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152001; AAF73197.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0030154; P:cell differentiation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000152; ASX_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR008297; Notch.
DR InterPro; IPR000800; Notch_dom.
DR InterPro; IPR001673; S_mold_repeat.
DR Pfam; PF00023; ank; 6.
DR Pfam; PF00008; EGF; 35.
DR Pfam; PF00066; notch; 3.
DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00011; EGF_LAMININ.
DR PRINTS; PR001452; NOTCH.
DR PRODOM; PDOM06869; S_mold_repeat; 1.
DR SMART; SMC0248; ANK; 6.
DR SMART; SMC0181; EGF; 35.
DR SMART; SMC0179; EGF_CA; 33.
DR SMART; SMC0004; NL; 3.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS00297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 22.

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DR PROSITE; PS00022; EGF\_1; 34.  
DR PROSITE; PS01186; EGF\_2; 30.  
DR PROSITE; PS01187; EGF\_3; 20.  
DR PROSITE; PS00038; HLH\_1; 1.  
DR PIRSF; PIRSF02279; Notch; 1.  
SQ SEQUENCE 2468 AA; 266643 MW; F147966714EP946B CRC64;

Alignment Scores:  
Pred. No.: 0.00942 Length: 2468  
Score: 102.50 Matches: 34  
Percent Similarity: 39.85% Conservative: 19  
Best Local Similarity: 25.58% Mismatches: 47  
Query Match: 11.54% Indels: 33  
DB: 13 Gaps: 9

US-09-773-476-294 (1-489) x Q800E4 (1-2468)  
QY 44 CCAAACTTTTACAGGCTTACTCTATTCATATAGAC---CTTCAGGCAAACTCTCTC 100  
Db 435 ProGlyTyRgInGlyTyRgCysGluValAspIleAspGluCysGluSerAsnProCys 454  
QY 101 AAGGAT-----GATTGGCCCAACCTTCCGT-----GGG 130  
Db 455 ValAsnAspGlyLeCysArgAspMetValAsnGlyPheThrCysThrCysGlnProGly 474  
QY 131 TTTACTCAGCTCAGACTCTGATCTACACAGATGTT-----CCC 172  
Db 475 PheThrGlyThrMetCysGlnIle-----AspIleAspGluCysAlaSerThrPro 491  
QY 173 TGCTCTGGAGGTAGTAATGCTGGGCAATGTTACTTCTTCAAG----- 217  
Db 492 CysGlnAsnGlyAlaLysCysIleAspArgProAsnGlyTyRgCysArgCysAlaGlu 511  
QY 218 -----GACAACAGATTGCGAAGGCAAGGACCTTTTGCATAGCACTGGAGGCCA 271  
Db 512 GlyPheGluGlyArgLeuGlyCysGluSerAsnIleAspAsnCys-----LysPro 527  
QY 272 GAAATGTGCTGAGAACGATCTGTGCATCTGACGGTCCTGTCCTTTTGCAGTGCCTT 331  
Db 528 AspProCys---HisHisGlyThrCysVal---AspGlyIleAlaSerTyRThrCysAsn 545  
QY 332 TGCTGTGATGTTTCCATGATACAGTGTATGAGGCAG 370  
Db 546 CysGluProGlyTyRThrGlyTyRArgCysGluAsnGln 558

RESULT 15  
O46370  
ID O46370 PRELIMINARY; PRT; 308 AA.  
AC O46370;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Preadipocyte factor-1.  
GN DLK.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fat;  
RA Minoshima Y., Taniguchi Y., Sasaki Y.;  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Fahrenkrug S.C., Freking B.A., Smith T.P.S.;  
RT "Genomic Organization and Chromosomal Position of the Bovine DLK  
Gene."  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB009278; BAA23733.1; -  
DR EMBL; AF181466; AAF00926.1; -  
DR EMBL; AF181463; AAF00926.1; JOINED.

Search completed: June 25, 2004, 09:16:14  
Job time : 50 secs









QY 128 GGGTTTACTCAGCTGAGACTCTGTATACCAAGAT----- 166  
Db 264 GlyPheThrGlyLeuAspCysGluMetAsnProAspAspCysValArgHisGlnCysGln 283  
QY 167 -----GTTCCCTGCTCGAGGTAGT 187  
Db 284 AsnGlyAlaThrCysLeuAspGlyLeuAspThrTyThrCysProCysProLysThrTrp 303  
QY 188 AATGCTGGGACAATGTTACTTCTTCAAGGACAAGCAGATTGGCAAGGGCAAGGAC 247  
Db 304 LysGlyTyrPasp-----CysSerGluAspIleAsp 313  
QY 248 CTTTCAATAGACACTGAGACCCAGAAATGCTCTGAGAACGATCTGTGATCTGAC 307  
Db 314 GluCysGluAlaArgGlyProProArg---CysA-gAsnGlyGlyThrCysGlnAsnThr 332  
QY 308 GGTCTCTGCTTTTTCAGTGCCTGTTGCTGATGTTTCCATGGATACAAAGTGTATG--- 364  
Db 333 Ala--GlySerPheHisCysValCysValSerGlyTyrGlyGlyAlaGlyCysGluGlu 351  
QY 365 -----AGGCAG 370  
Db 352 AsnLeuAspAspCysAlaAlaAlaThrCysAlaProGlySerThrCysIleAspArgVal 371  
QY 371 GGCTCATTTTCACTGCTTATGTTCTTTGGGA 401  
Db 372 GlySerPheSer-CysLeuCysProProGly 381

RESULT 5

US-08-537-210A-4  
; Sequence 4, Application US/08537210A  
; Patent No. 5780300  
; GENERAL INFORMATION:  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Fortini, Mark  
; APPLICANT: Matsuno, Kenji  
; TITLE OF INVENTION: MANIPULATION OF NON-TERMINALLY  
; TITLE OF INVENTION: DIFFERENTIATED CELLS USING THE NOTCH PATHWAY  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/537,210A  
; FILING DATE: 29-SEP-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7326-027  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1139 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Dros N

; LOCATION: 1189...2327  
; OTHER INFORMATION: Highly conserved ankyrin repeat  
; OTHER INFORMATION: region of No. 5780300ch  
US-08-537-210A-4

Alignment Scores:  
Pred. No.: 0.00408 Length: 1139  
Score: 102.00 Matches: 25  
Percent Similarity: 42.25% Conservative: 5  
Best Local Similarity: 35.21% Mismatches: 29  
Query Match: 11.49% Indels: 12  
DB: 1 Gaps: 3

US-09-773-476-294 (1-489) x US-08-537-210A-4 (1-1139)

QY 170 CCCTGTCTCTGAGGTAGTAATGCTGGGACAATGTTACTTCTTCAAGGACAAG----- 223  
Db 41 ProCysGlnAsnGlyGlyThrCysHisAspArgValMetAsnPheSerCysSerCysPro 60  
QY 224 -----CAGATTGCGAAGGCAAGGACCTTTGCAATAGCACTGGAAGC 268  
Db 61 ProGlyThrMetGlyIleIleCysGluIleAsnLysAspAspCys-----Lys 76  
QY 269 CCAGAAATGTCTCTGAGAACGGATCTTGTCATCTGACGGTCTGTGCTCTTTTGCAGTGC 328  
Db 77 ProGlyAlaCysHisAsnAsnGlySerCysIle---AspArgValGlyGlyPheGluCys 95  
QY 329 GTTTGCTGCTGATGTTTCCATGGATACAAAGTGT 361  
Db 96 ValCysGlnProGlyPheValGlyAlaArgCys 106

RESULT 6

US-09-113-825-4  
; Sequence 4, Application US/09113825  
; Patent No. 6149902  
; GENERAL INFORMATION:  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Fortini, Mark  
; APPLICANT: Matsuno, Kenji  
; TITLE OF INVENTION: MANIPULATION OF NON-TERMINALLY  
; TITLE OF INVENTION: DIFFERENTIATED CELLS USING THE NOTCH PATHWAY  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/113,825  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/537,210  
; FILING DATE: 29-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7326-027  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1139 amino acids  
; TYPE: amino acid

STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 FEATURE:  
 NAME/KEY: Dros N 2327  
 LOCATION: 1189-2327  
 OTHER INFORMATION: Highly conserved ankyrin repeat  
 OTHER INFORMATION: region of No. 6149902ch  
 US-09-113-825-4

Alignment Scores:  
 Pred. No.: 0.00408 Length: 1139  
 Score: 102.00 Matches: 25  
 Percent Similarity: 42.25% Conservativity: 5  
 Best Local Similarity: 35.21% Mismatches: 29  
 Query Match: 11.49% Indels: 12  
 DB: 3 Gaps: 3

US-09-773-476-294 (1-489) x US-09-113-825-4 (1-1139)

QY 170 CCTGTCTGGAGTAGTAATGCTGGACAATGTTACTTCTTCAAGGACAAG----- 223  
 Db 41 ProCysGlnAsnGlyGlyThrCysHisAspArgValMetAsnPheSerCysSerCysPro 60  
 QY 224 -----CAGATTTCGCAAGGCGCAAGGACCTTTGCAATACGACTGGAAGC 268  
 Db 61 ProGlyThrMetGlyIleIleCysGluIleAsnLysAspAspCys-----Lys 76  
 QY 269 CCAGAAATGTCTCGAAGCGATCTTGTGCATCTGACGGCTCTGTTTTCGAGTGC 328  
 Db 77 ProGlyAlaCysHisAsnAsnGlySerCysIle---AspArgValGlyGlyPheGluCys 95  
 QY 329 GTTTGTGCTGATGTTTCCATGGATACAAAGT 361  
 Db 96 ValCysGlnProGlyPheValGlyAlaArgCys 106

# RESULT 7

US-08-185-432-16  
 Sequence 16, Application US/08185432  
 Patent No. 5750652

## GENERAL INFORMATION:

APPLICANT: Artavanis-Tsakonas, Spyridon  
 APPLICANT: Busseau, Isabelle  
 APPLICANT: Diederich, Robert J.  
 APPLICANT: Xu, Tian  
 APPLICANT: Matsuno, Kenji  
 TITLE OF INVENTION: DELTA PROTEINS, NUCLEIC ACIDS, AND  
 TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PENNIE & EDMONDS  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-2711

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA: US/08/185,432

APPLICATION NUMBER: US/08/185,432  
 FILING DATE: 21-JAN-1994  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mistock, S. Leslie  
 REGISTRATION NUMBER: 18,872  
 REFERENCE/DOCKET NUMBER: 7326-006  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-8864/9741  
 TELEX: 66141 PENNIE

## INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 2471 amino acids  
 TYPE: amino acid  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 US-08-185-432-16

Alignment Scores:  
 Pred. No.: 0.0054 Length: 2471  
 Score: 102.00 Matches: 42  
 Percent Similarity: 36.18% Conservativity: 13  
 Best Local Similarity: 27.63% Mismatches: 48  
 Query Match: 11.49% Indels: 49  
 DB: 1 Gaps: 8

US-09-773-476-294 (1-489) x US-08-185-432-16 (1-2471)

QY 74 ATCATAGACTTCAGGCAATCCTCTCAAGGAT-----GATTGGCCCAAC 118  
 Db 912 IleAspAspCysLeuAlaAsnProCysGlnAsnGlyGlySerCysMetAspGlyValAsn 931  
 QY 119 ACCTTCCGT-----GGTTTACT-----CAGCTGCAGACTCTGATCTA 157  
 Db 932 ThrPheSerCysLeuCysLeuProGlyPheThrGlyAspLysCysGlnThr----- 948  
 QY 158 CCACAAGATGT-----CCCTGTCTCTGGAGGTAGTAAATGCTCTGGAC 199  
 Db 949 -----AspMetAsnGluCysLeuSerGluProCysLysAsnGlyGlyThrCysSerAsp 966  
 QY 200 AATGTTACTTCTTCAAGACACAGCAGATTTCACAAAGGCAAGGACCTTTGCAATAGC 259  
 Db 967 TyrValAsnSerTyrThrCysLys-----CysGlnAlaGlyPheAspGlyValHisCys 984  
 QY 260 ACTGGAAGCCCAAGAAATGTCCTGAG-----AACGGATCTTGTGCATCTGAC 307  
 Db 985 GluAsnAsnIleAsnGluCysThrGluSerSerCysPheAsnGlyGlyThrCysValAsp 1004  
 QY 308 GGTCTCTGCTCTTTTGCAGTCGCTTGTGCTGATGTTCCATGGATACAACTGATGAGG 367  
 Db 1005 GlyIleAsnSerPheSerCysLeuCysProValGlyPheThrGlySerPheCysLeuHis 1024  
 QY 368 CAG----- 370  
 Db 1025 GluIleAsnGluCysSerSerHisProCysLeuAsnGluGlyThrCysValAspGlyLeu 1044  
 QY 371 GGCTCATTTTCACTGCTTATGTTCTTTGGATTC 404  
 Db 1045 GlyThr-TyrArgCysSerCysProLeuGlyTyr 1055

# RESULT 8

US-08-083-590A-19  
 Sequence 19, Application US/08083590A  
 Patent No. 5786158

## GENERAL INFORMATION:

APPLICANT: Artavanis-Tsakonas, S. et al.  
 TITLE OF INVENTION: Therapeutic And Diagnostic Methods  
 TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And  
 TITLE OF INVENTION: Nucleic Acids  
 NUMBER OF SEQUENCES: 21  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/083,590A
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 8698864/9741
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2471 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-083-590A-19

Alignment Scores:
Pred. No.: 0.0054 Length: 2471
Score: 102.00 Matches: 42
Percent Similarity: 36.18% Conservative: 13
Best Local Similarity: 27.63% Mismatches: 48
Query Match: 11.49% Indels: 49
DB: 1 Gaps: 8

US-09-773-476-294 (1-489) x US-08-083-590A-19 (1-2471)
QY 74 ATCATAGACTTCAGCAAAATCTCTCAAGAT-----GATTGGCCCAAC 118
Db 912 IleAspAspCysLeuAlaAsnProCysGlnAsnGlySerCysMetAspGlyValAsn 931
QY 119 ACCTTCGGT-----GGGTTTACT-----CAGCTGCAGACTCTGATACTA 157
Db 932 ThrPheSerCysLeuCysLeuProGlyPheThrGlyAspLysCysGlnThr----- 948
QY 158 CCACAGATGTT-----CCCTGCTCTGGAGGTAGTAAATGCTGGGAC 199
Db 949 -----AspMetAsnGluCysLeuSerGluProCysLysAsnGlyThrCysSerAsp 966
QY 200 AATGTTACTCTTTCAGGACAGCAGATTGCCAAGGCAAGGACCTTTGCAATAGC 259
Db 967 TyrValAsnSerTyrThrCysLys-----CysGlnAlaGlyPheAspGlyValHisCys 984
QY 260 ACTGGAAGCCAGAAATGTGTCTCTGAG-----AACGGATCTTTGTGCATCTGAC 307
Db 985 GluAsnAsnIleAsnGluCysThrGluSerSerCysPheAsnGlyThrCysValAsp 1004
QY 308 GGTCTGCTGTTTTCAGTGGTGTGCTGATGTTTCCATGATGATGATGATGAGG 367
Db 1005 GlyIleAsnSerPheSerCysLeuCysProValGlyPheThrGlySerPheCysLeuHis 1024
QY 368 CAG----- 370
Db 1025 GluIleAsnGluCysSerSerHisProCysLeuAsnGluGlyThrCysValAspGlyLeu 1044

RESULT 9
US-08-532-384-19
; Sequence 19, Application US/08532384
; Patent No. 6083904
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S. et al.
; TITLE OF INVENTION: Therapeutic And Diagnostic Methods
; TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And
; TITLE OF INVENTION: Nucleic Acids
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
;
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,384
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/083,590
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2471 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-532-384-19

Alignment Scores:
Pred. No.: 0.0054 Length: 2471
Score: 102.00 Matches: 42
Percent Similarity: 36.18% Conservative: 13
Best Local Similarity: 27.63% Mismatches: 48
Query Match: 11.49% Indels: 49
DB: 1 Gaps: 8

US-09-773-476-294 (1-489) x US-08-532-384-19 (1-2471)
QY 74 ATCATAGACTTCAGCAAAATCTCTCAAGAT-----GATTGGCCCAAC 118
Db 912 IleAspAspCysLeuAlaAsnProCysGlnAsnGlySerCysMetAspGlyValAsn 931
QY 119 ACCTTCGGT-----GGGTTTACT-----CAGCTGCAGACTCTGATACTA 157
Db 932 ThrPheSerCysLeuCysLeuProGlyPheThrGlyAspLysCysGlnThr----- 948
QY 158 CCACAGATGTT-----CCCTGCTCTGGAGGTAGTAAATGCTGGGAC 199
Db 949 -----AspMetAsnGluCysLeuSerGluProCysLysAsnGlyThrCysSerAsp 966
QY 200 AATGTTACTCTTTCAGGACAGCAGATTGCCAAGGCAAGGACCTTTGCAATAGC 259
Db 967 TyrValAsnSerTyrThrCysLys-----CysGlnAlaGlyPheAspGlyValHisCys 984
QY 260 ACTGGAAGCCAGAAATGTGTCTCTGAG-----AACGGATCTTTGTGCATCTGAC 307
Db 985 GluAsnAsnIleAsnGluCysThrGluSerSerCysPheAsnGlyThrCysValAsp 1004
QY 308 GGTCTGCTGTTTTCAGTGGTGTGCTGATGTTTCCATGATGATGATGATGAGG 367
Db 1005 GlyIleAsnSerPheSerCysLeuCysProValGlyPheThrGlySerPheCysLeuHis 1024
QY 368 CAG----- 370
Db 1025 GluIleAsnGluCysSerSerHisProCysLeuAsnGluGlyThrCysValAspGlyLeu 1044
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QY 371 GGTCATTTCACGCTGATGTTCTTTGGGATTC 404  
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Db 1045 GlyThr-TyrArgCysSerCysProLeuGlyTyr 1055

## RESULT 10

US-08-899-232-1  
; Sequence 1, Application US/08899232  
; Patent No. 6436650  
; GENERAL INFORMATION:  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Oi, Huilin  
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON  
; FILE REFERENCE: 7326-046  
; CURRENT APPLICATION NUMBER: US/08/899,232  
; CURRENT FILING DATE: 1997-07-23  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 2471  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-899-232-1

Alignment Scores:  
Pred. No.: 0.0054 Length: 2471  
Score: 102.00 Matches: 42  
Percent Similarity: 36.18% Conservative: 13  
Best Local Similarity: 27.63% Mismatches: 48  
Query Match: 11.49% Indels: 49  
DB: 4 Gaps: 8

US-09-773-476-294 (1-489) x US-08-899-232-1 (1-2471)

QY 74 ATCATAGACCTTCAGGCAATCTCTCAAGAT-----GATTGGCCAAC 118  
| | | | | : : : | | | | | : : : | | | : :  
Db 912 ILeAspAspCysLeuAlaAsnProCysGlnAsnGlySerCysMetAspGlyValAsn 931  
| | | | | : : : | | | | | : : : | | | : :  
QY 119 ACCTTCGGT-----GGCTTTACT-----CAGCTGCAGACTCTGATACTA 157  
| | | | | : : : | | | | | : : : | | | : :  
Db 932 ThrPheSerCysLeuCysLeuProGlyPheThrGlyAspLysCysGlnThr----- 948  
| | | | | : : : | | | | | : : : | | | : :  
QY 158 CCACAGATGTT-----CCTGTCTCGAGGTAGTAGTAATGCTCGGAC 199  
| | | | | : : : | | | | | : : : | | | : :  
Db 949 -----AspMetAsnGluCysLeuSerGluProCysLysAsnGlyGlyThrCysSerAsp 966  
| | | | | : : : | | | | | : : : | | | : :  
QY 200 AATGTTACTTTCAGGACAGCAGATTTGCCAAGGGCAAGGACCTTTGCATAGC 259  
| | | | | : : : | | | | | : : : | | | : :  
Db 967 TyrValAsnSerTyrThrCysLys-----CysGlnAlaGlyPheAspGlyValHisCys 984  
| | | | | : : : | | | | | : : : | | | : :  
QY 260 ACTGGAAGCCACAGAAATGTCTCTGAG-----AACGGATCTTTGTGCATCTGAC 307  
| | | | | : : : | | | | | : : : | | | : :  
Db 985 GluAsnAsnIleAsnGluCysThrGluSerSerCysPheAsnGlyGlyThrCysValAsp 1004  
| | | | | : : : | | | | | : : : | | | : :  
QY 308 GGTCCTGGTCTTTGCAAGTGGTTTGCTGATGTTTCCATCGATACAGTGTATGAGG 367  
| | | | | : : : | | | | | : : : | | | : :  
Db 1005 GlyIleAsnSerPheSerCysLeuCysProValGlyPheThrGlySerPheCysLeuHis 1024  
| | | | | : : : | | | | | : : : | | | : :  
QY 368 CAG----- 370  
| | | | | : : : | | | | | : : : | | | : :  
Db 1025 GluIleAsnGluCysSerSerHisProCysLeuAsnGluGlyThrCysValAspGlyLeu 1044  
| | | | | : : : | | | | | : : : | | | : :  
QY 371 GGTCATTTCACGCTGATGTTCTTTGGGATTC 404  
| | | | | : : : | | | | | : : : | | | : :  
Db 1045 GlyThr-TyrArgCysSerCysProLeuGlyTyr 1055  
| | | | | : : : | | | | | : : : | | | : :

## RESULT 11

US-08-185-432-19  
; Sequence 19, Application US/08185432  
; Patent No. 5750652  
; GENERAL INFORMATION:  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Busseau, Isabelle  
; APPLICANT: Diederich, Robert J.

; APPLICANT: Xu, Tian  
; APPLICANT: Matsuno, Kenji  
; TITLE OF INVENTION: DEUTEROPROTEINS, NUCLEIC ACIDS, AND  
; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/185,432  
; FILING DATE: 21-JAN-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7326-006  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2703 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-185-432-19

Alignment Scores:  
Pred. No.: 0.0058 Length: 2703  
Score: 102.00 Matches: 25  
Percent Similarity: 42.25% Conservative: 5  
Best Local Similarity: 35.21% Mismatches: 29  
Query Match: 11.49% Indels: 12  
DB: 1 Gaps: 3

US-09-773-476-294 (1-489) x US-08-185-432-19 (1-2703)

QY 170 CCCTGTCTCTGGAGTAGTAATGCCTGGGACAATGTTACTTCTTCAAGGACAAG----- 223  
| | | | | : : : | | | | | : : : | | | : :  
Db 1229 ProCysGlnAsnGlyGlyThrCysHisAspArgValMetAsnPheSerCysSerCysPro 1248  
| | | | | : : : | | | | | : : : | | | : :  
QY 224 -----CAGATTTCGCAAGGGCAAGGACCTTTGCAATAGCACTGGAAGC 268  
| | | | | : : : | | | | | : : : | | | : :  
Db 1249 ProGlyThrMetGlyIlelleCysGluIleAsnLysAspAspCys-----Lys 1264  
| | | | | : : : | | | | | : : : | | | : :  
QY 269 CCAGAAATGTCTCTGAGACACGATCTTTGTGCARCTCGCTCCTGCTCTTTTGCAGTGC 328  
| | | | | : : : | | | | | : : : | | | : :  
Db 1265 ProGlyAlaCysHisAsnAsnGlySerCysile---AspArgValGlyGlyPheGluCys 1283  
| | | | | : : : | | | | | : : : | | | : :  
QY 329 GTTGTGCTGATGTTTCCATGATACAGTGT 361  
| | | | | : : : | | | | | : : : | | | : :  
Db 1284 ValCysGlnProGlyPheValGlyAlaArgCys 1294  
| | | | | : : : | | | | | : : : | | | : :

## RESULT 12

US-08-899-232-4  
; Sequence 4, Application US/08899232  
; Patent No. 6436650  
; GENERAL INFORMATION:  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Oi, Huilin  
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON  
; FILE REFERENCE: 7326-046  
; CURRENT APPLICATION NUMBER: US/08/899,232

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; CURRENT FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2703
; TYPE: PRI
; ORGANISM: Drosophila sp.
; US-08-899-232-4

Alignment Scores:
Pred. No.: 0.0058      Length: 2703
Score: 102.00          Matches: 25
Percent Similarity: 42.25%      Conservative: 5
Best Local Similarity: 35.21%    Mismatches: 29
Query Match: 11.49%             Indels: 12
DB: 4                        Gaps: 3

US-09-773-476-294 (1-489) x US-08-899-232-4 (1-2703)
QY 170 CCTGTCCTGGAGGTAGTAATGCTGGGACATGTTACTTCTTCAAGACAAG----- 223
Db 1229 ProCysGlnAsnGlyThrCysHisAspArgValMetAsnPheSerCysSerCysPro 1248
QY 224 -----CAGATTGGCAAGGGCAAGGACCTTTGCAATAGCACTGGAAGC 268
Db 1249 ProGlyThrMetGlyIleLeuGlyCysGluIleAsnLysAspCys-----Lys 1264
QY 269 CCAGAAATGTCCTGAGAACGGATCTTGTGCATCTGACGGTCCTGCTTTTTCGAGTGC 328
Db 1265 ProGlyAlaCysHisAsnAsnGlySerCysIle---AspArgValGlyGlyPheGluCys 1283
QY 329 GTTTCGTGCTGCTGCTTCCATGATACAACTGT 361
Db 1284 ValCysGlnProGlyPheValGlyAlaArgCys 1294

RESULT 13
US-08-185-432-17
; Sequence 17, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Busseau, Isabelle
; APPLICANT: Diederich, Robert J.
; APPLICANT: Xu, Tian
; APPLICANT: Matsuno, Kenji
; TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,432
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,972
; REFERENCE/DOCKET NUMBER: 7326-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 2556 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-185-432-17

Alignment Scores:
Pred. No.: 0.00715      Length: 2556
Score: 101.00          Matches: 41
Percent Similarity: 35.19%      Conservative: 16
Best Local Similarity: 25.31%    Mismatches: 54
Query Match: 11.37%             Indels: 51
DB: 1                        Gaps: 6

US-09-773-476-294 (1-489) x US-08-185-432-17 (1-2556)
QY 53 TTACAGCTTATATCTGCT-----ATTATCATAGACCTTCAG-----GCAATCTCT 97
Db 441 LeuGlnGlyThrGlyProArgCysGluIleAspValAsnGluCysValSerAsnPro 460
QY 98 CTCAAGGATGATTGGCCAAACACCTTCCTGGGTGTTTACTCAGCTGCAGACTCTGATACTA 157
Db 461 CysGlnAsnAsp---AlaThrCysLeuAspGluIleGlyGluPheGlnCysMetCysMet 479
QY 158 CCA-----CAAGATGTCCTCTGT 175
Db 480 ProGlyThrGluGlyValHisCysGluValAsnThrAspGluCysAlaSerSerProCys 499
QY 176 CCTGGAGGTAGTAATGCTGGGACATGTTACTTCTTCAAGGACAAG----- 223
Db 500 LeuHisAsnGlyArgCysLeuAspLysIleAsnGluPheGlnCysGluCysProThrGly 519
QY 224 -----CAGATTTCGCAAGGGCAAGGACCTTTGCAATAGCACTGGAAGCCAGAA 274
Db 520 PheThrGlyHisLeuCysGlnTyrAspValAspGluCysAlaSerThr----- 535
QY 275 ATGTGCTCTGAGAACGGATCTTGTGCATCTGACGGTCCTGCTCTTTTGCAGTGGCTTGT 334
Db 536 ProCys---LysAsnGlyAlaLysCysLeuAspGlyProAsnThrTyrThrCysValCys 554
QY 335 GCTGATGTTTCCATGATACAAAGTGT----- 361
Db 555 ThrGluGlyThrGlyThrHisCysGluValAspGluCysAspProAspPro 574
QY 362 -----ATGAGCAGGGCTCATTTTCACTGCTTATGTTCTTTGGG 400
Db 575 CysHisTyrGlySerCysLysAsp-GlyValAlaThrPheThrCysLeuCysArgProG1 594
QY 401 ATTC 404
Db 594 YTYR 595

RESULT 14
US-08-083-590A-20
; Sequence 20, Application US/08083590A
; Patent No. 5786158
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S. et al.
; TITLE OF INVENTION: Therapeutic And Diagnostic Methods
; TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And
; TITLE OF INVENTION: Nucleic Acids
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: Patent In Release #1.0, Version #1.25
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, CURRENT APPLICATION DATA:
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, APPLICATION NUMBER: US/08/083,590A
, FILING DATE: 25-JUN-1993
, CLASSIFICATION: 435
, ATTORNEY/AGENT INFORMATION:
,
, NAME: Misrock, S. Leslie
, REGISTRATION NUMBER: 18,872
, REFERENCE/DOCKET NUMBER: 7326-015
, TELECOMMUNICATION INFORMATION:
,
, TELEPHONE: 212 790-9090
, TELEFAX: 212 8698964/9741
, TELEX: 66141 PENNIE
,
, INFORMATION FOR SEQ ID NO: 20:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 2556 amino acids
, TYPE: amino acid
, STRANDEDNESS: single
, TOPOLOGY: unknown
, MOLECULE TYPE: peptide
,
, US-08-083-590A-20

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Alignment Scores:	0.00715	Length:	2556
Fred. No.:	101.00	Matches:	41
Score:	35.19%	Conservative:	16
Percent Similarity:	25.31%	Mismatches:	54
Best Local Similarity:	11.37%	Indels:	51
Query Match:	1	Gaps:	8
DB:			

US-09-773-476-294 (1-489) x US-08-083-590A-20 (1-2556)

QY	53	TTACAGGCTTATAC	TGCT-----ATTATCATAGACCTTCAG-----GCATATCCT	97
Db	441	LeuGlnGlyTyrThrGlyProArgCysgluIleAspValAsnGluCysValSerAsnPro	460	
QY	98	CTCAGGATGATTTGGCCCAACACACCTTCGGTGGGTTTACTCAGCTGCAGACTCTGATACPA	157	
Db	461	CysGlnAsnAsp---AlaThrCysLeuAspGlnIleGluPheGlnCysMetCysMet	479	
QY	158	CCA-----CAAGATGTTCCCTGT	175	
Db	480	ProGlyTyrGluGlyValHisCysgluValAsnThrAspGluCysAlaSerSerProCys	499	
QY	176	CCTGGAGGTAGTAATGCCTGGAGCAAGTACTTCTTTCAAGGACAAG-----	223	
Db	500	LeuHisAsnGlyArgCysLeuAspIysIleAsnGluPheGlnCysGluCysProThrGly	519	
QY	224	-----CAGATTGCGCAAGGCAAGGACCTTTGCAATAGCACTGGAGCCCAAG	274	
Db	520	PheThrGlyHisLeuCysGlnTyrAspValAspGluCysAlaSerThr-----	535	
QY	275	ATGTGTCCTGAGAACGGATCTTGTCATCTGACGCTCTGCTTTTGCAAGTCGGTTGT	334	
Db	536	ProCys---LysAsnGlyAlaIysCysLeuAspGlyProAsnThrTyrThrCysValCys	554	
QY	335	GCTGATGGTTCCATGGGATACAAGTGT-----	361	
Db	555	ThrGluGlyTyrThrGlyThrHisCysgluValAspIleAspGluCysAspProAspPro	574	
QY	362	-----ATGAGGCAGGGCTCATTTCACTGCTTATGTTCTTTGGG	400	
Db	575	CysHisTyrGlySerCysLysAsp-GlyValAlaIaThrPheThrCysLeuCysArgProG	594	
QY	401	ATTC	404	
Db	594	yTyr	595	

RESULT 15  
 US-08-532-384-20  
 ; Sequence 20, Application US/08532384  
 Patent No. 6083904

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/ GENERAL INFORMATION:
/ APPLICANT: Artavanis-Tsakonas, S. et al.
/ TITLE OF INVENTION: Therapeutic And Diagnostic Methods
/ TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And
/ TITLE OF INVENTION: Nucleic Acids
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/532,384
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/083,590
/ FILING DATE: 25-JUN-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Misrock, S. Leslie
/ REGISTRATION NUMBER: 18,872
/ REFERENCE/DOCKET NUMBER: 7326-015
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212 790-9090
/ TELEFAX: 212 8698864/9741
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2556 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/
US-08-532-384-20

Alignment Scores:
Fred. No.: 0.00715 Length: 2556
Score: 101.00 Matches: 41
Percent Similarity: 35.19% Conservative: 16
Best Local Similarity: 25.31% Mismatches: 54
Query Match: 51 Indels: 51
DR. 3 Gaps: 8

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US-09-773-476-294 (1-489) x US-08-532-384-20 (1-2556)

Qy	53	TTACAGGCTTATCTGCT	-----ATTATCATGACCTTCAG	-----GCAATCT	97
Db	441	LeuGlnGlyTyrThrGlyProArgCysGluIleAspValAsnGluCysValSerAsnPro			460
Qy	98	CTCAGGATGTTGGCCAAACCTCCCGTGGCTTACTCAGCTGCAGACTCTGATACTA			157
Db	461	CysGlnAsnAsp---AlaThrCysLeuaspGlnIleGlyGluPheGlnCysMetCysMet			479
Qy	158	CCA	-----CAAGATGTTCCCTGT	-----	175
Db	480	ProGlyTyrGluGlyValHisCysGluValAsnThrAspGluCysAlaSerSerProCys			499
Qy	176	CCTGGAGGTAGTAATGCCTGGGCAAGTACTTCTTTCAAGGACAAG			223
Db	500	LeuHisAsnGlyArgCysLeuaspIlyIleAsnGluPheGlnCysGluCysProThrGly			519
Qy	224	-----CRAGTTTGCAGGGCAAGGACCTTTGCAATAGACTTGGAGCCACAGA			274
Db	520	PheThrGlyHisLeuCysGlnTyr-AspValAspGluCysAlaSerThr			535
Qy	275	ATGTGTCCTGAGAACCGATCTTTGGCATCTGACGGTCCTGGTCTTTTGACAGTCGGTTGT			334



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Db      536 ProCys---LysAsnGlyAlaLysCysLeuAspGlyProAsnThrTyrThrCysValCys 554
QY      335 GCTGATGGTTCCATGGATACAAAGTCT----- 361
Db      555 ThrGluGlyTyrThrGlyThrHisCysGluValAspIleAspGluCysAspProAspPro 574
QY      362 -----ATGAGGCAGGGCTCATTTCACCTGCTTATGTTCTTTGGG 400
Db      575 CysHisTyrGlySerCysLysAsp-GlyValAlaThrPheThrCysLeuCysArgProG1 594
QY      401 ATTC 404
Db      594 yTyr 595

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004. Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 25, 2004, 09:13:58 ; Search time 44.5 Seconds  
(without alignments)  
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Title: US-09-773-476-294

Perfect score: 888

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Ygapop 10.0, Ygapext 0.5

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Delopt 6.0, Delopt 7.0

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 2327084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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41	690	77.7	229	14	US-10-243-425-8	Sequence 8, Appli
42	690	77.7	229	14	US-10-243-446-8	Sequence 8, Appli
43	690	77.7	229	14	US-10-245-874-8	Sequence 8, Appli
44	690	77.7	229	14	US-10-242-653-8	Sequence 8, Appli
45	690	77.7	229	14	US-10-243-167-8	Sequence 8, Appli

#### ALIGNMENTS

RESULT 1  
US-09-726-348-2  
; Sequence 2, Application US/09726348  
; Patent No. US200202553A1  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Ying-Fei  
; APPLICANT: et al,  
; TITLE OF INVENTION: Transforming Growth Factor Alpha HIII  
; FILE OF INVENTION: PF220PI  
; CURRENT APPLICATION NUMBER: US/09/726,348  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: 08/778,545  
; PRIOR FILING DATE: 1997-01-03  
; PRIOR APPLICATION NUMBER: 60/011,136  
; PRIOR FILING DATE: 1996-01-04  
; PRIOR APPLICATION NUMBER: 60/168,387  
; PRIOR FILING DATE: 1999-12-02  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 229  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-726-348-2

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Alignment Scores:
Pred. No.: 3 51e-65 Length: 229
Score: 690.00 Matches: 128
Percent Similarity: 89.68% Conservative: 11
Best Local Similarity: 82.58% Mismatches: 16
Query Match: 77.70% Indels: 1
DB: 9 Gaps: 0

US-09-773-476-294 (1-489) x US-09-726-348-2 (1-229)
QY 3 CTGAGGCTAGATCTTCAGAACTGTCCTT-CAGAGTCTGCTGTCACAACTTTTACAGGCT 61
DB 73 LeuGlyLeuAspLeuGlnAsnSerLeuGluAspProGlyProAsnPheHisGlnAla 92
QY 62 TATAGTCTATTATCATAGACCTTCAGGCAATCTCTCAAGGATGATTGGCCACACC 121
DB 93 HisThrThrValIleLeuAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaThr 112
QY 122 TTCGCTGGTTCATCTAGCTGACACTCTGATCTACTACCAAGATGTTCCCTGCTGGA 181
DB 113 PheArgGlyPheThrGlnLeuGlnThrLeuIleLeuProGlnHisValAsnCysProGly 132
QY 182 GGTAGTAAATGCTGGGCAATGTTACTCTTTCAGGACAAAGCAGATTTGCCAAGGCAA 241
DB 133 GlyIleAsnAlaTrpAsnThrIleThrSerTyrlleAspAsnGlnIleCysGlnGlyGln 152
QY 242 AGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTCTGAGAACGGAATCTTGCA 301
DB 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172
QY 302 TCTGACGCTGCTGCTTTTTCAGTGGGAACTTCTGCTGCTGCTGCTGCTGCTGCTGCT 361
DB 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrlsCys 192
QY 362 ATGAGGAGGCTGCTATTTTCACTGCTTATGTTCTTGGGATTCGGATCCACAGCTA 421
DB 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrLeu 212
QY 422 GCCATCTNCAATCTTACTTTGGGAACTTGGGAACTTGGGAACTTGGGAACTTGGGAA 466
DB 213 SerValSerIleLeuLeuTrpAlaThrGlnArgGlyAlaLys 227

RESULT 2
US-10-245-752-8
; Sequence 8, Application US/10245752
; Publication No. US20030064473A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C66
; CURRENT APPLICATION NUMBER: US/10/245,752
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10

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; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 8
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-245-752-8

Alignment Scores:
Pred. No.: 3 51e-65 Length: 229
Score: 690.00 Matches: 128
Percent Similarity: 89.68% Conservative: 11
Best Local Similarity: 82.58% Mismatches: 16
Query Match: 77.70% Indels: 1
DB: 9 Gaps: 0

US-09-773-476-294 (1-489) x US-10-245-752-8 (1-229)
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QY 62 TATAGTCTATTATCATAGACCTTCAGGCAATCTCTCAAGGATGATTGGCCACACC 121
DB 93 HisThrThrValIleLeuAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaThr 112
QY 122 TTCGCTGGTTCATCTAGCTGACACTCTGATCTACTACCAAGATGTTCCCTGCTGGA 181
DB 113 PheArgGlyPheThrGlnLeuGlnThrLeuIleLeuProGlnHisValAsnCysProGly 132
QY 182 GGTAGTAAATGCTGGGCAATGTTACTCTTTCAGGACAAAGCAGATTTGCCAAGGCAA 241
DB 133 GlyIleAsnAlaTrpAsnThrIleThrSerTyrlleAspAsnGlnIleCysGlnGlyGln 152
QY 242 AGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTCTGAGAACGGAATCTTGCA 301
DB 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172
QY 302 TCTGACGCTGCTGCTTTTTCAGTGGGAACTTCTGCTGCTGCTGCTGCTGCTGCTGCT 361
DB 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrlsCys 192
QY 362 ATGAGGAGGCTGCTATTTTCACTGCTTATGTTCTTGGGATTCGGATCCACAGCTA 421
DB 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrLeu 212
QY 422 GCCATCTNCAATCTTACTTTGGGAACTTGGGAACTTGGGAACTTGGGAACTTGGGAA 466
DB 213 SerValSerIleLeuLeuTrpAlaThrGlnArgGlyAlaLys 227

RESULT 3
US-10-245-859-8
; Sequence 8, Application US/10245859
; Publication No. US20030064474A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin

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; PRIOR APPLICATION NUMBER: 60/123618  
; PRIOR FILING DATE: 1999-03-10  
; PRIOR APPLICATION NUMBER: 60/131294  
; PRIOR FILING DATE: 1999-04-07  
; PRIOR APPLICATION NUMBER: 60/140650  
; PRIOR FILING DATE: 1999-06-22  
; PRIOR APPLICATION NUMBER: 60/141037  
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; PRIOR APPLICATION NUMBER: 60/144758  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 60/162506  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: 60/170262  
; PRIOR FILING DATE: 1999-12-09  
; PRIOR APPLICATION NUMBER: 60/187202  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: 60/209832  
; PRIOR FILING DATE: 2000-06-05  
; PRIOR APPLICATION NUMBER: 60/232887  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: 09/180997  
; PRIOR FILING DATE: 1998-11-19  
; PRIOR APPLICATION NUMBER: 09/218517  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: 09/284291  
; PRIOR FILING DATE: 1999-04-12  
; PRIOR APPLICATION NUMBER: 09/380137  
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; PRIOR FILING DATE: 1999-11-10  
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; PRIOR APPLICATION NUMBER: 09/802706  
; PRIOR FILING DATE: 2001-03-09  
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; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 09/872035  
; PRIOR FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: 09/882636  
; PRIOR FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 09/924419  
; PRIOR FILING DATE: 2001-08-06  
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; PRIOR FILING DATE: 2001-08-06  
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; PRIOR APPLICATION NUMBER: 09/946374  
; PRIOR FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: PCT/US98/18824  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: PCT/US99/00106  
; PRIOR FILING DATE: 1999-01-05  
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; PRIOR APPLICATION NUMBER: PCT/US99/12252  
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; PRIOR APPLICATION NUMBER: PCT/US99/20111  
; PRIOR FILING DATE: 1999-09-01  
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; PRIOR FILING DATE: 1999-09-08  
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; PRIOR FILING DATE: 1999-12-02  
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; PRIOR FILING DATE: 2000-08-11  
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; PRIOR APPLICATION NUMBER: PCT/US00/30873  
; PRIOR FILING DATE: 2000-11-10  
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; PRIOR APPLICATION NUMBER: PCT/US01/06666  
; PRIOR FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: PCT/US01/17092  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: PCT/US01/17800  
; PRIOR FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: PCT/US01/19692  
; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: PCT/US01/21066  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: PCT/US01/21735  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: PCT/US01/27099  
; PRIOR FILING DATE: 2001-08-29  
; NUMBER OF SEQ ID NOS: 91  
; SEQ ID NO 2  
; LENGTH: 229  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-001-054-2  
  
Alignment Scores:  
Pred. No.: 3, Size-65 Length: 229  
Score: 690.00 Matches: 128  
Percent Similarity: 89.68% Conservative: 11  
Best Local Similarity: 82.58% Mismatches: 16  
Query Match: 77.70% Indels: 1  
DB: 13 Gaps: 0  
  
US-09-773-476-294 (1-489) x US-10-001-054-2 (1-229)  
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Db 93 HisThrThrValIleileAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112
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Qy 302 TCTGACGGTCCGTCGCTTTTGCAGTCCGTTGCTGCTGATGTTTCCATGGATACAGGTGT 361
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Qy 362 ATGAGCGAGGCTCATTTTCACTGCTTATGTTCTTTGGGATCTGGATCCACACGCTA 421
Db 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212
Qy 422 GCCATCTNCATTTCTACTTTGGGAAAGCCAGCCGCGGAAAGCCAAAG 466
Db 213 SerValSerIleLeuLeuTrpAlaThrGlnArgArgLysAlaLys 227
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## RESULT 5

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US-10-245-103-8
; Sequence 8, Application US/10245103
; Publication No. US20030068779A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C112
; CURRENT APPLICATION NUMBER: US/10/245,103
; PRIOR FILING DATE: 2002-09-17
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 8
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-103-8
Alignment Scores:
Pred. No.: 3,51e-65 Length: 229
Score: 690.00 Matches: 128
Percent Similarity: 89.68% Conservative: 11
Best Local Similarity: 82.58% Mismatches: 16
Query Match: 77.70% Indels: 1
DB: 14 Gaps: 0
US-09-773-476-294 (1-489) x US-10-245-103-8 (1-229)
Qy 3 CTGAGGCTAGACTCTCAGAACTGTTCCT-GAGGATCTGGTCCAAACTTTTACAGCT 61
Db 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92
Qy 62 TATACCTGCTATTATCATAGACCTTCAGGCAAAATCTCTCAAGGATGATTGGCCAAACACC 121
Db 93 HisThrThrValIleileAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112
Qy 122 TTCGGTGGGTTTACTCAGCTGAGACTCTGATCTACTACACAAAGATGTTCCCTGCTCTGGA 181
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Qy 242 AGGACCTTTGCAATAGCACTGGAAGCCCAAGATGTTCTTCAAGGCAAGCAGATTTGCCAAGGCAA 301
Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172
Qy 302 TCTGACGGTCCGTCGCTTTTGCAGTCCGTTGCTGCTGATGTTTCCATGGATACAGGTGT 361
Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrllysCys 192
Qy 362 ATGAGCGAGGCTCATTTTCACTGCTTATGTTCTTTGGGATCTGGATCCACACGCTA 421
Db 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212
Qy 422 GCCATCTNCATTTCTACTTTGGGAAAGCCAGCCGCGGAAAGCCAAAG 466
Db 213 SerValSerIleLeuLeuTrpAlaThrGlnArgArgLysAlaLys 227
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## RESULT 6

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; Sequence 8, Application US/10245107
; Publication No. US20030068779A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C171
; CURRENT APPLICATION NUMBER: US/10/245,107
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
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; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 8
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-107-8

Alignment Scores:
Pred. No.: 3 51e-65 Length: 229
Score: 690.00 Matches: 128
Percent Similarity: 89.68% Conservative: 11
Best Local Similarity: 82.58% Mismatches: 16
Query Match: 77.70% Indels: 1
DB: 14 Gaps: 0

US-09-773-476-294 (1-489) x US-10-245-107-8 (1-229)
QY 3 CTGAGGCTAGATCTTCAGACTGTCCT-CAGGATCCTGGTCCAACTTTTACAGGCT 61
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Db 213 SerValSerIleLeuLeuTrpAlaThrGlnArgArgLysAlaLys 227

RESULT 7
US-10-245-143-8
; Sequence 8, Application US/10245143
; Publication No. US20030068780A1
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Fillaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C90
; CURRENT APPLICATION NUMBER: US/10/245,143
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 8
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-143-8
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Alignment Scores:
Pred. No.: 3 51e-65 Length: 229
Score: 690.00 Matches: 128
Percent Similarity: 89.68% Conservative: 11
Best Local Similarity: 82.58% Mismatches: 16
Query Match: 77.70% Indels: 1
DB: 14 Gaps: 0

US-09-773-476-294 (1-489) x US-10-245-143-8 (1-229)
QY 3 CTGAGGCTAGATCTTCAGACTGTCCT-CAGGATCCTGGTCCAACTTTTACAGGCT 61
Db 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92
QY 62 TATAGTCTATTATCATAGACCTTCAGGCAAACTCTCAAGGATGATTTGGCCACACC 121
Db 93 HisThrThrValIleLeuAspLeuGlnAlaAsnProLeuGlyAspLeuAlaAsnThr 112
QY 122 TTCGGTGGTTTACTCAGCTGACACTCTGATACCAAGATGTTCCCTGCTCTGGA 181
Db 113 PheArgGlyPheThrGlnLeuGlnThrLeuLeuProGlnHisValAsnCysProGly 132
QY 182 GGTAGTAATGCTGGGACAATGTTACTTCTTCAAGGACAAGCAGATTTCGCAAGGCCAA 241
Db 133 GlyIleAsnAlaTrpAsnThrIleThrSerTyrIleAspAsnGlnIleCysGlnGlyGln 152
QY 242 AGGACCTTTTGCAATGACATGGAAGCCCAAGAAATGTCCTGAGAACGATCTTGTCGA 301
```



Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172  
Qy 302 TCTGACGGTCTGCTGCTTTTGCAGTGGCTTTGCTGCTGATGTTCCATGGATACAAAGTGT 361  
Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys 192  
Qy 362 ATGAGCGAGGCTCATTTTCACTGCTTATGTTCTTTGGGATTCGGGATCCACACAGCTA 421  
Db 193 MetAsgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212  
Qy 422 GCCATCTNCAATCTACTTTGGGAAACCCAGCGCCGGAAGCAAG 466  
Db 213 SerValSerIleLeuLeuTrpAlaThrGlnArgAsgLysAlaLys 227

RESULT 8  
US-10-245-771-8  
; Sequence 8, Application US/10245771  
; Publication NO. US20030068781A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C98  
; CURRENT APPLICATION NUMBER: US/10/245, 771  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; LENGTH: 229  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-245-771-8

Alignment Scores:  
Pred. No.: 3,51e-65  
Score: 690.00  
Matches: 128  
Conservative: 11  
Best Local Similarity: 89.68%  
Query Match: 82.58%  
Indels: 16  
Gaps: 1  
DB: 0

US-09-773-476-294 (1-489) x US-10-245-771-8 (1-229)  
Qy 3 CTGAGGCTAGATCTTCTGAGACTGTTCCCT- GAGGATCTGCTGCTCAAACTTTTACAGGCT 61  
Db 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92  
Qy 62 TATAGTCTATTATCATAGACCTTTCAGGCAAAATCCCTCTCAAGGATGATTGGCCAAACACC 121  
Db 93 HisThrThrValIleIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112  
Qy 122 TTCGCTGGGTTTACTGAGCTGAGACTCTGATCTATCTACCAAGCAGATTTCCCAAGGSCAA 181  
Db 113 PheArgGlyPheThrGlnLeuGlnThrLeuIleLeuProGlnHisValAsnCysProGly 132  
Qy 182 GGTAGTAATCCCTGGGCAAAATGTTACTTCTTCAAGCAACAGCAGATTTCCCAAGGSCAA 241  
Db 133 GlyIleAsnAlaTrpAsnThrIleThrSerTyrIleAspAsnGlnIleCysGlnGlyGln 152  
Qy 242 AGGACCTTTTGCATAGCCTGGAAGCCAGAAATGTCTCTGAGAACGGATCTTGTGCA 301  
Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172  
Qy 302 TCTGACGGTCTGCTGCTTTTGCAGTGGCTTTGCTGCTGATGCTTCCATGGATACAAAGTGT 361  
Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys 192  
Qy 362 ATGAGCGAGGCTCATTTTCACTGCTTATGTTCTTTGGGATTCGGGATCCACACAGCTA 421  
Db 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212  
Qy 422 GCCATCTNCAATCTACTTTGGGAAACCCAGCGCCGGAAGCAAG 466  
Db 213 SerValSerIleLeuLeuTrpAlaThrGlnArgLysAlaLys 227

RESULT 9  
US-10-245-851-8  
; Sequence 8, Application US/10245851  
; Publication NO. US20030068782A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C93  
; CURRENT APPLICATION NUMBER: US/10/245, 851  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557

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/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 8
/ LENGTH: 229
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-851-8

Alignment Scores:
Pred. No.: 3,51e-65 Length: 229
Score: 690.00 Matches: 128
Percent Similarity: 89.68% Conservative: 11
Best Local Similarity: 82.58% Mismatches: 16
Query Match: 77.70% Indels: 1
DB: 14 Gaps: 0

US-09-773-476-294 (1-489) x US-10-245-851-8 (1-229)
Qy 3 CTGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCCTGGTCCAAACTTTTACAGGCT 61
Db 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92
Qy 62 TATACTGCTATTATCATAGACCTTCAGGAAATCCTCTCAAGGATGATTTGGCCAAACACC 121
Db 93 HisThrThrValIleIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112
Qy 122 TTCGCTGGGTTTACTCAGCTGCAGACTCTGATACCTACCAAGATGTTCCCTGCTCGGA 181
Db 113 PheArgGlyPheThrGlnLeuGlnThrLeuIleLeuProGlnHisValAsnCysProGly 132
Qy 182 GGTAGTAATGCTGGGACAATGTTACTTCTTCAAGCAAGCAGATTTGCCAAGGCCAA 241
Db 133 GlyIleAsnAlaThrAsnThrIleThrSerTyIleAspAsnGlnIleCysGlnGlyGln 152
Qy 242 AGGACCTTTGCATACACCTGGAAGCCAGAAATGTCCTGAGACCGATCTTGTGCA 301
Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172
Qy 302 TCTGACGCTCCTGGTCTTTTGCAGTGGTTGTGCTGATGGTTTCCATGGATACAGTGT 361
Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyLysCys 192
Qy 362 ATGAGGAGGGCTCATTTTCACTGCTTATGTTCTTTGGGATCTTGGATCCACCGCTA 421
Db 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212
Qy 422 GCCATCTNCATTTCTACTTTGGGAAACCCAGCGCGGAAAGCCCAAG 466
Db 213 SerValSerIleLeuLeuTrpAlaThrGlnArgArgLysAlaLys 227
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## RESULT 10

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US-10-245-883-8
/ Sequence 8, Application US/10245883
/ Publication No. US20030068783A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Eaton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Phillippe
/ APPLICANT: Watanabe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zhenmin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3630R1C70
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/ CURRENT APPLICATION NUMBER: US/10/245,883
/ CURRENT FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 8
/ LENGTH: 229
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-883-8

Alignment Scores:
Pred. No.: 3,51e-65 Length: 229
Score: 690.00 Matches: 128
Percent Similarity: 89.68% Conservative: 11
Best Local Similarity: 82.58% Mismatches: 16
Query Match: 77.70% Indels: 1
DB: 14 Gaps: 0

US-09-773-476-294 (1-489) x US-10-245-883-8 (1-229)
Qy 3 CTGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCCTGGTCCAAACTTTTACAGGCT 61
Db 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92
Qy 62 TATACTGCTATTATCATAGACCTTCAGGAAATCCTCTCAAGGATGATTTGGCCAAACACC 121
Db 93 HisThrThrValIleIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112
Qy 122 TTCGCTGGGTTTACTCAGCTGCAGACTCTGATACCTACCAAGATGTTCCCTGCTCGGA 181
Db 113 PheArgGlyPheThrGlnLeuGlnThrLeuIleLeuProGlnHisValAsnCysProGly 132
Qy 182 GGTAGTAATGCTGGGACAATGTTACTTCTTCAAGCAAGCAGATTTGCCAAGGCCAA 241
Db 133 GlyIleAsnAlaThrAsnThrIleThrSerTyIleAspAsnGlnIleCysGlnGlyGln 152
Qy 242 AGGACCTTTGCATACACCTGGAAGCCAGAAATGTCCTGAGACCGATCTTGTGCA 301
Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172
Qy 302 TCTGACGCTCCTGGTCTTTTGCAGTGGTTGTGCTGATGGTTTCCATGGATACAGTGT 361
Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyLysCys 192
Qy 362 ATGAGGAGGGCTCATTTTCACTGCTTATGTTCTTTGGGATCTTGGATCCACCGCTA 421
Db 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212
Qy 422 GCCATCTNCATTTCTACTTTGGGAAACCCAGCGCGGAAAGCCCAAG 466
Db 213 SerValSerIleLeuLeuTrpAlaThrGlnArgArgLysAlaLys 227
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## RESULT 11

US-10-237-535-8  
; Sequence 8, Application US/10237535  
; Publication No. US20030073188A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Pong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3630RIC3  
; CURRENT APPLICATION NUMBER: US/10/237,535  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079669  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-03-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: 60/091358  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/099803  
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; PRIOR APPLICATION NUMBER: 60/106932  
; PRIOR FILING DATE: 1998-11-03  
; PRIOR APPLICATION NUMBER: 60/115554  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/119342  
; PRIOR FILING DATE: 1999-02-09  
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; PRIOR FILING DATE: 1999-03-12  
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; PRIOR FILING DATE: 1999-04-27  
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; PRIOR APPLICATION NUMBER: 60/138385  
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; PRIOR APPLICATION NUMBER: 60/140653  
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; PRIOR FILING DATE: 1999-06-23  
; PRIOR APPLICATION NUMBER: 60/144732  
; PRIOR FILING DATE: 1999-07-20  
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; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 60/144790  
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; PRIOR APPLICATION NUMBER: 60/145228  
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; PRIOR APPLICATION NUMBER: 60/145698  
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; PRIOR APPLICATION NUMBER: 60/170262  
; PRIOR FILING DATE: 1999-12-09  
; PRIOR APPLICATION NUMBER: 60/177118  
; PRIOR FILING DATE: 2000-01-20  
; PRIOR APPLICATION NUMBER: 60/179851  
; PRIOR FILING DATE: 2000-02-02  
; PRIOR APPLICATION NUMBER: 60/180921  
; PRIOR FILING DATE: 2000-02-08  
; PRIOR APPLICATION NUMBER: 60/187202  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: 60/198587  
; PRIOR FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: 60/199614  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 60/206330  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/206368  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/209832  
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; PRIOR APPLICATION NUMBER: 60/218371  
; PRIOR FILING DATE: 2000-07-13  
; PRIOR APPLICATION NUMBER: 60/222695  
; PRIOR FILING DATE: 2000-08-02  
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; PRIOR APPLICATION NUMBER: 60/230621  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/232887  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: 60/235147  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 60/261878  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 60/261910  
; PRIOR FILING DATE: 2001-01-16  
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; PRIOR APPLICATION NUMBER: 60/262150  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 60/264395

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4	PRIOR APPLICATION NUMBER: 607267623	
5	PRIOR FILING DATE: 2001-02-09	
6	PRIOR APPLICATION NUMBER: 607274399	
7	PRIOR FILING DATE: 2001-03-09	
8	PRIOR APPLICATION NUMBER: 607280982	
9	PRIOR FILING DATE: 2001-04-03	
10	PRIOR APPLICATION NUMBER: 607282129	
11	PRIOR FILING DATE: 2001-04-04	
12	PRIOR APPLICATION NUMBER: 607282199	
13	PRIOR FILING DATE: 2001-04-04	
14	PRIOR APPLICATION NUMBER: 607290588	
15	PRIOR FILING DATE: 2001-05-09	
16	PRIOR APPLICATION NUMBER: 09/180997	
17	PRIOR FILING DATE: 1998-11-19	
18	PRIOR APPLICATION NUMBER: 09/267213	
19	PRIOR FILING DATE: 1999-03-12	
20	PRIOR APPLICATION NUMBER: 09/380137	
21	PRIOR FILING DATE: 1999-08-25	
22	PRIOR APPLICATION NUMBER: 09/380138	
23	PRIOR FILING DATE: 1999-08-25	
24	PRIOR APPLICATION NUMBER: 09/403297	
25	PRIOR FILING DATE: 1999-10-18	
26	PRIOR APPLICATION NUMBER: 09/423741	
27	PRIOR FILING DATE: 1999-11-10	
28	PRIOR APPLICATION NUMBER: 09/709238	
29	PRIOR FILING DATE: 2000-11-08	
30	PRIOR APPLICATION NUMBER: 09/802706	
31	PRIOR FILING DATE: 2001-03-09	
32	PRIOR APPLICATION NUMBER: 09/872035	
33	PRIOR FILING DATE: 2001-06-01	
34	PRIOR APPLICATION NUMBER: 09/918585	
35	PRIOR FILING DATE: 2001-07-30	
36	PRIOR APPLICATION NUMBER: 09/924419	
37	PRIOR FILING DATE: 2001-08-06	
38	PRIOR APPLICATION NUMBER: 09/927796	
39	PRIOR FILING DATE: 2001-08-09	
40	PRIOR APPLICATION NUMBER: 09/929404	
41	PRIOR FILING DATE: 2001-08-13	
42	PRIOR APPLICATION NUMBER: 09/931836	
43	PRIOR FILING DATE: 2001-08-16	
44	PRIOR APPLICATION NUMBER: 09/941992	
45	PRIOR FILING DATE: 2001-08-28	
46	PRIOR APPLICATION NUMBER: 09/946374	
47	PRIOR FILING DATE: 2001-09-04	
48	PRIOR APPLICATION NUMBER: 10/001054	
49	PRIOR FILING DATE: 2001-11-30	
50	PRIOR APPLICATION NUMBER: 10/052586	
51	PRIOR FILING DATE: 2002-01-15	
52	PRIOR APPLICATION NUMBER: 10/081056	
53	PRIOR FILING DATE: 2002-02-20	
54	PRIOR APPLICATION NUMBER: 10/119480	
55	PRIOR FILING DATE: 2002-04-09	

Alignment Scores:		
Pred. No.:	3,510-65	Length:
Score:	690.00	Matches:
Percent Similarity:	89.6%	Conservative:
Best Local Similarity:	82.5%	Mismatches:
Query Match:	77.70%	Indels:
DB:	14	Gaps:
		229
		128
		11
		16
		1
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US-09-773-476-294 (1-489) x US-10-237-535-8 (1-229)

QY	3	CTGAGGCTAGATCTTCAGAACTGTTCCCT	-GAGGATCTGGTCCAACTTTTTACAGGCT	61
Db	73	LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla	92	
QY	62	TATACTGCTATTATCATGACCTTCAGCAAACTCTCTCAAGGATGATTTGGCCAACACC	121	
Db	93	HisThrThrValIleLeuAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr	112	

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122  TTCCGTTGGGTTTACTCAGCTCTCAGACTCTGTGATCTACTACCAAGAGATGTTCCCTGTCTCTGGA 181
123  PheArgGlyPheThrGlnLeuGlnThrLeuLeuLeuProGlnHisValAsnCysProGly 132
124  GGTACTGATGCTCTGGCAACAATGTTACTTCTTCAAGGACAAGCAGAGATTTGCCAAGGGCAA 241
125  GlyIleAsnAlaTpaAsnThrIleThrSerTyrIleAspAsnGlnIleCysGlnGlyGln 152
126  AGGACCTTTTGCATATGACACTGTGGAGCCGACAGAAATGTCTCTGAGAACGGATCTTGTGCA 301
127  LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172
128  TCTGACGGTCTCTGGTCTTTTTCAGTGGGTTTGTGCTGATGGTTTCCATGGATACAAGTGT 361
129  ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrIysCys 192
130  ATGAGGACGGGCTCATTTTCACTGCTTATGTTCTTTGGGATCTTGGATCCACACAGCTTA 421
131  MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212
132  GCACCTTCATCTTACTTCTTGGGGAACCCAGCGCGGGAARGCCAAG 466
133  SerValSerIleLeuLeuTpaAlaThrGlnArgLysAlaIys 227

RESULT 12
US-10-238-183-8
; Sequence 8, Application US/10238183
; Publication No. US20030073189A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

```

APPLICANT: FONG, SHEIMIAN  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

PRIOR APPLICATION NUMBER: 60/106932  
PRIOR FILING DATE: 1998-11-03  
PRIOR APPLICATION NUMBER: 60/115554  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/119342  
PRIOR FILING DATE: 1999-02-09  
PRIOR APPLICATION NUMBER: 60/123957  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/123972  
PRIOR FILING DATE: 1999-03-11  
PRIOR APPLICATION NUMBER: 60/127372  
PRIOR FILING DATE: 1999-04-01  
PRIOR APPLICATION NUMBER: 60/131271  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/133459  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/135725  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: 60/135729  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: 60/135750  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: 60/138385  
PRIOR FILING DATE: 1999-06-09  
PRIOR APPLICATION NUMBER: 60/140653  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: 60/141037  
PRIOR FILING DATE: 1999-06-23  
PRIOR APPLICATION NUMBER: 60/144732  
PRIOR FILING DATE: 1999-07-20  
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PRIOR APPLICATION NUMBER: 60/146222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: 60/146843  
PRIOR FILING DATE: 1999-08-03  
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PRIOR FILING DATE: 1999-08-12  
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PRIOR APPLICATION NUMBER: 60/162506  
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PRIOR APPLICATION NUMBER: 60/170262  
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PRIOR APPLICATION NUMBER: 60/179851  
PRIOR FILING DATE: 2000-02-02  
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PRIOR APPLICATION NUMBER: 60/187202  
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PRIOR FILING DATE: 2000-04-18  
PRIOR APPLICATION NUMBER: 60/199614  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 60/206330  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/206368  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/209832  
PRIOR FILING DATE: 2000-06-05  
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PRIOR FILING DATE: 2000-07-13  
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PRIOR FILING DATE: 2000-08-02  
PRIOR APPLICATION NUMBER: 60/229896  
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PRIOR APPLICATION NUMBER: 60/230521  
PRIOR FILING DATE: 2000-09-05  
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PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: 60/235147  
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PRIOR FILING DATE: 2001-02-02  
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PRIOR FILING DATE: 2001-03-09  
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PRIOR FILING DATE: 2001-04-03  
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PRIOR FILING DATE: 2001-04-04  
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PRIOR FILING DATE: 2001-05-09  
PRIOR APPLICATION NUMBER: 09/180997  
PRIOR FILING DATE: 1998-11-19  
PRIOR APPLICATION NUMBER: 09/267213  
PRIOR FILING DATE: 1999-03-12  
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PRIOR APPLICATION NUMBER: 09/403297  
PRIOR FILING DATE: 1999-10-18  
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PRIOR FILING DATE: 1999-11-10  
PRIOR APPLICATION NUMBER: 09/709238  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 09/802706  
PRIOR FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: 09/872035  
PRIOR FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 09/924419  
PRIOR FILING DATE: 2001-08-06  
PRIOR APPLICATION NUMBER: 09/927796  
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PRIOR FILING DATE: 2001-08-13  
PRIOR APPLICATION NUMBER: 09/931836  
PRIOR FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: 09/941992  
PRIOR FILING DATE: 2001-08-28  
PRIOR APPLICATION NUMBER: 09/946374  
PRIOR FILING DATE: 2001-09-04

;; PRIOR APPLICATION NUMBER: 10/001054  
;; PRIOR FILING DATE: 2001-11-30  
;; PRIOR APPLICATION NUMBER: 10/052586  
;; PRIOR FILING DATE: 2002-01-15  
;; PRIOR APPLICATION NUMBER: 10/081056  
;; PRIOR FILING DATE: 2002-02-20  
;; PRIOR APPLICATION NUMBER: 10/119480  
;; PRIOR FILING DATE: 2002-04-09

Alignment Scores:  
Pred. No.: 3 51e-65 Length: 229  
Score: 690.00 Matches: 128  
Percent Similarity: 89.68% Conservativity: 11  
Best Local Similarity: 82.58% Mismatches: 16  
Query Match: 77.70% Indels: 1  
DB: 14 Gaps: 0

US-09-773-476-294 (1-489) x US-10-238-183-8 (1-229)

QY 3 CTGAGGCTAGATCTTCAGACTGTTCCCT-CAGGATCCTGGTCCAAACTTTTACAGGCT 61  
Db 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92  
QY 62 TATAGTCTATTATCATAGACCTTCAGGCAAACTCTCAAGGATGATTGGCCAAACAC 121  
Db 93 HisThrThrValIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112  
QY 122 TTCGCTGGGTTTACTAGCTGCAGACTCTGATATCTACCAAGATGTTCCCTGTCTGGA 181  
Db 113 PheArgGlyPheThrGlnLeuGlnThrLeuLeuProGlnHisValAsnCysProGly 132  
QY 182 GGTAGTAAATGCTGGGCAATGTTACTTCTTCAAGCAAGACAGATTTGCCAAGGCA 241  
Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172  
QY 302 TCTGACGCTCCTGCTTTTGAGTGGTGTGCTGATGCTTCCATGATACAGTGT 361  
Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys 192  
QY 362 ATGAGCAGGCTCATTTTCACTGCTTATGTTCTTTGGGATCTTGGGATCCACCGCTA 421  
Db 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyLeuGlyAlaThrThrLeu 212  
QY 422 GCATCTNCATTTACTTTGGGAAACCCAGCGCGGAAAGCCAAAG 466  
Db 213 SerValSerIleLeuLeuTrpAlaThrGlnArgArgLysAlaLys 227

RESULT 13  
US-10-238-283-8  
; Sequence 8, Application US/10238283  
; Publication No. US20030073190A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3630R1C15  
; CURRENT APPLICATION NUMBER: US/10/238,283  
; CURRENT FILING DATE: 2002-09-09

;; PRIOR APPLICATION NUMBER: 10/197942  
;; PRIOR FILING DATE: 2002-07-18  
;; PRIOR APPLICATION NUMBER: 60/059114  
;; PRIOR FILING DATE: 1997-09-17  
;; PRIOR APPLICATION NUMBER: 60/063046  
;; PRIOR FILING DATE: 1997-10-24  
;; PRIOR APPLICATION NUMBER: 60/065027  
;; PRIOR FILING DATE: 1997-11-10  
;; PRIOR APPLICATION NUMBER: 60/079689  
;; PRIOR FILING DATE: 1998-03-27  
;; PRIOR APPLICATION NUMBER: 60/086478  
;; PRIOR FILING DATE: 1998-05-22  
;; PRIOR APPLICATION NUMBER: 60/087607  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/089801  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/090557  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090689  
;; PRIOR FILING DATE: 1998-06-25  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 116  
;; SEQ ID NO 8  
;; LENGTH: 229  
;; TYPE: PRT  
;; ORGANISM: Homo Sapien  
US-10-238-283-8

Alignment Scores:  
Pred. No.: 3 51e-65 Length: 229  
Score: 690.00 Matches: 128  
Percent Similarity: 89.68% Conservativity: 11  
Best Local Similarity: 82.58% Mismatches: 16  
Query Match: 77.70% Indels: 1  
DB: 14 Gaps: 0

US-09-773-476-294 (1-489) x US-10-238-283-8 (1-229)

QY 3 CTGAGGCTAGATCTTCAGACTGTTCCCT-CAGGATCCTGGTCCAAACTTTTACAGGCT 61  
Db 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92  
QY 62 TATAGTCTATTATCATAGACCTTCAGGCAAACTCTCAAGGATGATTGGCCAAACAC 121  
Db 93 HisThrThrValIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112  
QY 122 TTCGCTGGGTTTACTAGCTGCAGACTCTGATATCTACCAAGATGTTCCCTGTCTGGA 181  
Db 113 PheArgGlyPheThrGlnLeuGlnThrLeuLeuProGlnHisValAsnCysProGly 132  
QY 182 GGTAGTAAATGCTGGGCAATGTTACTTCTTCAAGCAAGACAGATTTGCCAAGGCA 241  
Db 133 GlyIleAsnAlaTrpAsnThrIleThrSerTy-IleAspAsnGlnIleCysGlnGlyGln 152  
QY 242 AGGACCTTTGCAATAGACTGGAAGCCAGAAATGTCTCCTGAGAACCGATCTTGCA 301  
Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172  
QY 302 TCTGACGCTCCTGCTCTTTTGAGTGGTGTGCTGATGCTTCCATGATACAGTGT 361  
Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys 192  
QY 362 ATGAGCAGGCTCATTTTCACTGCTTATGTTCTTTGGGATCTTGGGATCCACCGCTA 421  
Db 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212  
QY 422 GCATCTNCATTTACTTTGGGAAACCCAGCGCGGAAAGCCAAAG 466  
Db 213 SerValSerIleLeuLeuTrpAlaThrGlnArgArgLysAlaLys 227

RESULT 14  
US-10-238-370-8  
; Sequence 8, Application US/10238370

Publication No. US20030073191A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3630R1C10  
; CURRENT APPLICATION NUMBER: US/10/238,370  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 8  
; LENGTH: 229  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-238-370-8  
  
Alignment Scores:  
Pred. No.: 3 51e-65 Length: 229  
Score: 690.00 Matches: 128  
Percent Similarity: 89.68% Conservative: 11  
Best Local Similarity: 82.58% Mismatches: 16  
Query Match: 77.70% Indels: 1  
DB: 14 Gaps: 0  
  
US-09-773-476-294 (1-489) x US-10-238-370-8 (1-229)  
QY 3 CTGAGCTAGACTTCAGAACTGTTCCCT-GAGGATCTCGTGCCAACTTTTACAGCT 61  
Db 73 LeuGlyLeuAspLeuGlnAsnSerLeuGluAspProGlyProAsnPheHisGlnAla 92  
QY 62 TATACGCTATATATACAGCTTCAGCAATCTCTCAAGGATGATTGGCCACACC 121  
Db 93 HisThrThrValIleLeuAspLeuGlnAlaAsnProLeuGlyAspLeuAlaAsnThr 112  
QY 122 TTCGGTGGTTTACTCAGCTGAGACTCTGATCTACCAAGATGTTCCCTGTCTCTGGA 181  
Db 113 PheArgGlyPheThrGlnLeuGlnThrLeuIleLeuProGlnHisValAsnSerProGly 132  
QY 182 GGTAGTAATGCTGGACAACTTACTTCTTTCAGGACAAACAGATTTGCCAAGGGA 241  
Db 133 GlyIleAsnAlaIleAsnThrIleThrSerTyrIleAsnGlnIleCysGlnGlyGln 152

QY 242 AGGACCTTTGCAATAGACTGGAGCCAGAAATGTCTCTGAGAACGGATCTTGTCGA 301  
Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172  
QY 302 TCTGACGGTCTCTGCTCTTTTTCAGTGGCTTTGTCTGCTGATGTTTCCATGGATACAAGTGT 361  
Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys 192  
QY 362 ATGAGGAGGGCTCATTTTCTACTCTTATGTTCTTCTGGGATTTCTGGGATCCACACGCTA 421  
Db 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212  
QY 422 GCCATCTNCATTTCTACTTTGGGAAACCCAGCGCGGAAAGCAAG 466  
Db 213 SerValSerIleLeuLeuThrAlaThrGluArgArgLysAlaLys 227  
  
RESULT 15  
US-10-245-055-8  
; Sequence 8, Application US/10245055  
; Publication No. US20030073192A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3630R1C88  
; CURRENT APPLICATION NUMBER: US/10/245,055  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
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; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 8  
; LENGTH: 229  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-245-055-8  
  
Alignment Scores:  
Pred. No.: 3 51e-65 Length: 229  
Score: 690.00 Matches: 128  
Percent Similarity: 89.68% Conservative: 11  
Best Local Similarity: 82.58% Mismatches: 16  
Query Match: 77.70% Indels: 1  
DB: 14 Gaps: 0

US-09-773-476-294 (1-489) x US-10-245-055-8 (1-229)

Qy	3	CTGAGGCTAGATCTTCAGAACTGTCCT-GAGGATCCTGGTCCAAACTTTTACAGGCT	61
Db	73	LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla	92
Qy	62	TATACTCTATTATCATAGACCTTCAGGCAAAATCCTCTCAAGGATGATTGGCCAAACCC	121
Db	93	HisThrThrValIleAspLeuGlnAlaAsnProLeuLysGlyLeuAlaAsnThr	112
Qy	122	TTCCGTGGGTTTACTCAGCTGCAGACTCTGATCTACTACCAAGATGTTCCCTGCTCTGGA	181
Db	113	PheArgGlyPheThrGlnLeuGlnThrLeuIleLeuProGlnHisValAsnCysProGly	132
Qy	182	GGTAGTAATGCTGGGACAATGTTACTTCTTCAAGGACAAGCAGATTTGCCAAGGGCAA	241
Db	133	GlyIleAsnAlaTrpAsnThrIleThrSeryIleAspAsnGlnIleCysGlnGln	152
Qy	242	AGGACCTTTGCATAGCACTGGAGCCAGAAATGTCTCTGAGAACGGATCTTGTGCA	301
Db	153	LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal	172
Qy	302	TCTCACGGTCTCTGTCTTTTGCAGTGGCTTTGTGCTGATGGTTTCCATGGATACAAGTGT	361
Db	173	ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys	192
Qy	362	ATGAGCAGGGCTCATTTTCACTGCTTATGTTCTTTGGGATCTGGATCCACACGCTA	421
Db	193	MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu	212
Qy	422	GCCATCTNCATTTCTTGGGAAACCAGCGCGGAAGCCAAAG	466
Db	213	SerValSerIleLeuLeuTrpAlaThrGlnArgLysAlaLys	227

Search completed: June 25, 2004, 09:19:32  
Job time : 47.5 secs